

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2004, 12:21:36 ; Search time 37.3949 Seconds
(without alignments)
1795.466 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
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- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
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- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
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- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | Length | DB | ID | Description |
|---------------|--------|------------|--|--------|----|----------|--------------------|
| | | Match | | | | | |
| 1 | 2407 | 100.0 | | 448 | 19 | AAW79739 | Human EEGF protein |
| 2 | 2407 | 100.0 | | 448 | 20 | AAW95709 | Homo sapiens fetal |
| 3 | 2407 | 100.0 | | 448 | 20 | AAW94281 | Human extracellula |
| 4 | 2407 | 100.0 | | 448 | 21 | AAY57058 | Amino acid sequenc |
| 5 | 2407 | 100.0 | | 448 | 21 | AAY54989 | Full length human |
| 6 | 2407 | 100.0 | | 448 | 22 | AAM93573 | Human polypeptide, |
| 7 | 2407 | 100.0 | | 448 | 23 | AAU75494 | Human extracellula |
| 8 | 2401 | 99.8 | | 448 | 20 | AAY08063 | Human EGF-like hom |
| 9 | 2401 | 99.8 | | 448 | 22 | AAU29227 | Human PRO polypept |
| 10 | 2401 | 99.8 | | 448 | 22 | AAB31183 | Amino acid sequenc |
| 11 | 2401 | 99.8 | | 448 | 24 | ABU71315 | Human PRO210 prote |
| 12 | 2401 | 99.8 | | 448 | 24 | ABU72040 | Novel human secret |
| 13 | 2401 | 99.8 | | 448 | 24 | ABU65772 | Human secreted/tra |
| 14 | 2401 | 99.8 | | 448 | 24 | ABU66105 | Novel human secret |
| 15 | 2401 | 99.8 | | 448 | 24 | ABU67141 | Novel human secret |
| 16 | 2401 | 99.8 | | 448 | 24 | ABU67272 | Novel human secret |
| 17 | 2401 | 99.8 | | 448 | 24 | ABU67609 | Human secreted/tra |
| 18 | 2401 | 99.8 | | 448 | 24 | ABU65467 | Human PRO polypept |
| 19 | 2401 | 99.8 | | 448 | 24 | ABU58603 | Human PRO polypept |
| 20 | 2401 | 99.8 | | 448 | 24 | ABU56139 | Human secreted/tra |
| 21 | 2401 | 99.8 | | 448 | 24 | ABU57134 | Human PRO polypept |
| 22 | 2401 | 99.8 | | 448 | 24 | ABU10713 | Human secreted/tra |
| 23 | 2302 | 95.6 | | 423 | 21 | AAY56751 | Smooth muscle prol |
| 24 | 2302 | 95.6 | | 423 | 21 | AAY56753 | Smooth muscle prol |
| 25 | 2302 | 95.6 | | 448 | 21 | AAY56750 | Smooth muscle prol |
| 26 | 2302 | 95.6 | | 448 | 21 | AAY54990 | Full length mouse |
| 27 | 2302 | 95.6 | | 461 | 21 | AAY56752 | Smooth muscle prol |
| 28 | 2302 | 95.6 | | 461 | 21 | AAY54991 | Full length mouse |
| 29 | 2230 | 92.6 | | 392 | 18 | AAW31705 | Human extracellula |
| 30 | 1827 | 75.9 | | 335 | 21 | AAY76008 | Rat EGF extracellu |
| 31 | 1827 | 75.9 | | 335 | 22 | AAB55947 | Skin cell protein, |
| 32 | 1827 | 75.9 | | 335 | 23 | ABB72147 | Rat protein isolat |
| 33 | 1276.5 | 53.0 | | 443 | 18 | AAW32110 | Human extracellula |
| 34 | 1276.5 | 53.0 | | 443 | 20 | AAY16587 | Extracellular prot |
| 35 | 1276.5 | 53.0 | | 443 | 21 | AAB33418 | Human PRO226 prote |
| 36 | 1276.5 | 53.0 | | 443 | 21 | AAY84707 | A human p53 mutant |
| 37 | 1276.5 | 53.0 | | 443 | 21 | AAY55850 | Human S1-5 ECMP-li |
| 38 | 1276.5 | 53.0 | | 443 | 22 | AAU12330 | Human PRO226 polyp |
| 39 | 1276.5 | 53.0 | | 443 | 23 | AAU86130 | Human PRO226 polyp |
| 40 | 1276.5 | 53.0 | | 443 | 24 | ABU66728 | Human PRO polypept |
| 41 | 1276.5 | 53.0 | | 443 | 24 | ABU67004 | Human secreted/tra |
| 42 | 1276.5 | 53.0 | | 443 | 24 | ABU59809 | Novel secreted and |
| 43 | 1272.5 | 52.9 | | 443 | 21 | AAY84706 | Amino acid sequenc |
| 44 | 1270.5 | 52.8 | | 443 | 22 | AAB92533 | Human protein sequ |
| 45 | 1237.5 | 51.4 | | 433 | 21 | AAB58353 | Lung cancer associ |

ALIGNMENTS

RESULT 1

AAW79739

ID AAW79739 standard; Protein; 448 AA.

XX

AC AAW79739;

XX

DT 25-JAN-1999 (first entry)

XX

DE Human EEGF protein.

XX

KW Extracellular/epidermal growth factor-like protein; EEGF; human; liver;
 KW vascular smooth muscle cell proliferation; neurology; pathology; AIDS;
 KW dementia; ocular; disorder; cornea; inflammation; tumour cell; kidney;
 KW wound; epithelium; surgery; skin graft; ulcer; diabetic; trophic;
 KW Marfan syndrome; treatment; hair follicle; embryogenesis; neoplasma;
 KW epidermal cell; cancer; psoriasis; detection.

XX

OS Homo sapiens.

XX

| | | |
|----|-----|---------------------|
| FH | Key | Location/Qualifiers |
|----|-----|---------------------|

| | | |
|----|---------|-------|
| FT | Peptide | 1..25 |
|----|---------|-------|

| | | |
|----|--|----------------|
| FT | | /label= signal |
|----|--|----------------|

| | | |
|----|---------|---------|
| FT | Protein | 26..448 |
|----|---------|---------|

| | | |
|----|--|--------------|
| FT | | /label= EEGF |
|----|--|--------------|

| | | |
|----|--|--|
| FT | | /note= "Extracellular/epidermal growth factor-like protein" |
|----|--|--|

| | | |
|----|--------|----------|
| FT | Region | 112..153 |
|----|--------|----------|

| | | |
|----|--|---------------|
| FT | | /label= EGF-1 |
|----|--|---------------|

| | | |
|----|--------|----------|
| FT | Region | 154..190 |
|----|--------|----------|

| | | |
|----|--|---------------|
| FT | | /label= EGF-2 |
|----|--|---------------|

| | | |
|----|--------|----------|
| FT | Region | 191..230 |
|----|--------|----------|

| | | |
|----|--|---------------|
| FT | | /label= EGF-3 |
|----|--|---------------|

| | | |
|----|--------|----------|
| FT | Region | 231..271 |
|----|--------|----------|

| | | |
|----|--|---------------|
| FT | | /label= EGF-4 |
|----|--|---------------|

| | | |
|----|--------|----------|
| FT | Region | 272..314 |
|----|--------|----------|

| | | |
|----|--|---------------|
| FT | | /label= EGF-5 |
|----|--|---------------|

XX

PN WO9846746-A1.

XX

PD 22-OCT-1998.

XX

PF 11-APR-1997; 97WO-US06020.

XX

PR 11-APR-1997; 97WO-US06020.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Li H, Olsen HS;

XX

DR WPI; 1998-568728/48.

DR N-PSDB; AAV62432.

XX

PT New isolated extracellular/epidermal growth factor - used for
 PT regulating vascular smooth muscle cell proliferation, e.g. for
 PT enhancing neurological functions or treating neoplasia and other
 PT disorders.

XX

PS Claim 10a; Fig 1A-D; 62pp; English.

XX

CC This sequence represents a novel human extracellular/epidermal growth
CC factor-like protein, EEGF. This protein can be used to regulate
CC vascular smooth muscle cell proliferation and for restoration or
CC enhancement of neurological functions diminished as a result or other
CC damaging pathologies such as AIDS dementia. The protein can also be used
CC to treat senile dementia, ocular disorders such as corneal inflammation,
CC for targeting tumour cells, for treating kidney disorders, for liver
CC regeneration or treating liver dysfunction, for treating wounds including
CC all cutaneous wounds, corneal wounds, and injuries to the
CC epithelial-lined hollow organs of the body or resulting from trauma such
CC as burns, abrasions and cuts as well as from surgical procedures such as
CC surgical incisions and skin grafting. The polypeptides can also be used
CC for treating chronic conditions, such as chronic ulcers, diabetic ulcers,
CC other non-healing (trophic) conditions, to treat Marfan syndrome, to
CC promote hair follicular development, to stimulate growth and
CC differentiation of various epidermal and epithelial cells in vivo and in
CC vitro and to stimulate embryogenesis. Antagonists to EEGF can be used to
CC treat neoplasia such as cancers or tumours, skin disorders such as
CC psoriasis or corneal inflammation. The products can also be used for
CC identifying EEGF receptors, detection, diagnosis and drug screening.

XX

SQ Sequence 448 AA;

Query Match 100.0%; Score 2407; DB 19; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.2e-159;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS | 60 |
| | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS | 85 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPQTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPQTQICI | 145 |
| Qy | 121 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 180 |
| | | | |
| Db | 146 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 205 |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQ | 240 |
| | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 300 |
| | | | |
| Db | 266 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 325 |
| Qy | 301 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKS | 360 |
| | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 |
| | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 |

Qy 421 YPF 423
|||
Db 446 YPF 448

RESULT 2

AAW95709

ID AAW95709 standard; Protein; 448 AA.

XX

AC AAW95709;

XX

DT 21-JUN-1999 (first entry)

XX

DE Homo sapiens fetal kidney clone AK647 secreted protein.

XX

KW Secreted protein; fetal kidney.

XX

OS Homo sapiens.

XX

PN WO9900405-A1.

XX

PD 07-JAN-1999.

XX

PF 29-JUN-1998; 98WO-US13530.

XX

PR 30-JUN-1997; 97US-0885610.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, Mccoy JM;

PI Merberg D, Racie LA, Treacy M;

XX

DR WPI; 1999-095671/08.

DR N-PSDB; AAX07567.

XX

PT New polynucleotides encoding secreted human proteins - are derived
PT from foetal kidney or adult retina cDNA libraries, used as, e.g.
PT potential vaccines

XX

PS Claim 11; Pages 52-54; 76pp; English.

XX

CC The sequence is that of a secreted protein from a human fetal
CC kidney clone AK296. Such a sequence is predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals, although no
CC supporting data is given. Suggested activities include nutritional
CC activity, cytokine and cell proliferation/differentiation activity,
CC immune stimulating (e.g. as vaccines) or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, and tumour
CC inhibition activity. It is also stated to be useful for gene
CC therapy.

XX

SQ Sequence 448 AA;

Query Match 100.0%; Score 2407; DB 20; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.2e-159;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | | | |
|----|-----|----------------------------|--|------------------|----|
| Qy | 1 | QCTNGFDLDRQSGQCLDI | DECRTIPEACRGDMMCVNQNGGYLCI | PRTNPVYRGPYSNPYS | 60 |
| | | | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDI | DECRTIPEACRGDMMCVNQNGGYLCI | PRTNPVYRGPYSNPYS | 85 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTI | SRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI | 120 | |
| | | | | | |
| Db | 86 | TPYSGPYPAAPPLSAPNYPTI | SRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI | 145 | |
| Qy | 121 | NTEGGYTCSCTDGYWLLEGQCLDI | DECYGYCQQLCANVPGSYSCTCNP | 180 | |
| | | | | | |
| Db | 146 | NTEGGYTCSCTDGYWLLEGQCLDI | DECYGYCQQLCANVPGSYSCTCNP | 205 | |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFI | CRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 240 | |
| | | | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSFI | CRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 | |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCQDINE | CEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 300 | |
| | | | | | |
| Db | 266 | PGTYFCSCPPGYILLDDNRSCQDINE | CEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 325 | |
| Qy | 301 | RISDNRCMCPAENPGCRDQPF | TILYRDMDVVSGRSVPADIFQM | 360 | |
| | | | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPF | TILYRDMDVVSGRSVPADIFQM | 385 | |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPI | KGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 | |
| | | | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPI | KGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 | |
| Qy | 421 | YPF | 423 | | |
| | | | | | |
| Db | 446 | YPF | 448 | | |

RESULT 3

AAW94281

ID AAW94281 standard; Protein: 448 AA.

XX

AC AAW94281;

XX

DT 07-MAY-1999 (first entry)

XX

DE Human extracellular matrix protein (ECMP)-1.

XX

KW Extracellular matrix protein; ECMP-1; diagnosis; treatment; cancer;

KW immune disorder; human.

XX

OS Homo sapiens.

XX

PN WO9900410-A2.

XX

PD 07-JAN-1999.

XX

PF 23-JUN-1998; 98WO-US13012.

XX
 PR 27-JUN-1997; 97US-0884072.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Bandman O, Corley NC, Guegler KJ;
 XX
 DR WPI; 1999-095674/08.
 DR N-PSDB; AAX05359.
 XX
 PT New polynucleotide encoding extracellular matrix protein, ECMP-1 -
 PT useful in the diagnosis, prevention and treatment of immune
 PT disorders and cancer
 XX
 PS Claim 1; Fig 1A-G; 79pp; English.
 XX
 CC This represents a human extracellular matrix protein (ECMP)-1. Host
 CC cells containing a vector comprising the ECMP-1 nucleic acid are used
 CC for the recombinant production of the protein. ECMP-1 and its
 CC (ant)agonists, are useful in the diagnosis, prevention, and treatment
 CC of cancer and immune disorders.
 XX
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2407; DB 20; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.2e-159;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 60 |
| | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 85 |
| Qy | 61 | TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHCNPTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHCNPTQICI | 145 |
| Qy | 121 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 180 |
| | | | |
| Db | 146 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 205 |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 240 |
| | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 300 |
| | | | |
| Db | 266 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 325 |
| Qy | 301 | RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQUATTRYPGAYYIFQIKS | 360 |
| | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQUATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 |
| | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 |
| Qy | 421 | YPF | 423 |

Db

|||
446 YPF 448

RESULT 4

AAAY57058

ID AAY57058 standard; Protein; 448 AA.

XX

AC AAY57058;

XX

DT 21-FEB-2000 (first entry)

XX

DE Amino acid sequence of the human secreted protein AK647.

XX

KW AK647; aortic tissue development; smooth muscle cell modulator; SCID;
KW nutritional supplement; vasculogenesis; embryonic development; infection;
KW cytokine activity; cell proliferation; cell differentiation; detect; HIV;
KW immune deficiency; haematopoiesis regulation; tissue regrowth; diagnose;
KW wound healing; restenosis; atherosclerosis; drug screen.

XX

OS Homo sapiens.

XX

PN WO9960125-A2.

XX

PD 25-NOV-1999.

XX

PF 18-MAY-1999; 99WO-US10931.

XX

PR 19-MAY-1998; 98US-0081002.

PR 21-MAY-1998; 98US-0083002.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, Racie L, LaVallie E, Treacy M, Evans C;
PI Agostino M, Lu Z, Merberg D;

XX

DR WPI; 2000-053298/04.

DR N-PSDB; AAZ39892.

XX

PT Proteins, and their encoding polynucleotides, used for treating e.g.
PT smooth muscle cell growth, vasculogenesis, restenosis or
PT atherosclerosis -

XX

PS Claim 4; Page 46-47; 49pp; English.

XX

CC This is the amino acid sequence of the human secreted protein AK647. The
CC polynucleotide sequence was obtained from a human foetal kidney cDNA
CC library. AK647 homologues in chicks and rodents are involved in aortic
CC tissue development. The spatial and temporal distribution of AK647
CC indicated that it acts as an a modulator of smooth muscle cells in
CC vasculogenesis during embryonic development. The primary structure of
CC AK647 consists of multiple EGF domains. The AK647 protein can be used as
CC a nutritional source or supplement. The protein shows both inhibitory and
CC inducing, cytokine, cell proliferation and cell differentiation activity.
CC The protein may also be used in the treatment of immune deficiencies and
CC disorders, including severe combined immunodeficiency (SCID), HIV and
CC other viral, bacterial and fungal infections. Regulation of immune

XX
 AC AAY54989;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Full length human A55 protein sequence.
 XX
 KW A55 protein; human; smooth muscle proliferation; tissue generation;
 KW vascular smooth muscle cell; arteriosclerosis; tissue reparation; myoma;
 KW vascular endothelial thickening; haematopoietic cell-regulator; cytokine;
 KW percutaneous transluminal coronary angioplasty; blood coagulation; PTCA;
 KW actin; inhibin; chemotaxis; thrombosis; cadherin; therapy;
 KW tumour metastasis inhibitor.
 XX
 OS Homo sapiens.
 XX
 PN WO9955864-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 28-APR-1999; 99WO-JP02284.
 XX
 PR 28-APR-1998; 98JP-0119731.
 XX
 PA (ONOEY) ONO PHARM CO LTD.
 XX
 PI Honjo T, Tashiro K, Nakamura T;
 XX
 DR WPI; 2000-038647/03.
 DR N-PSDB; AAZ40027.
 XX
 PT Novel human polypeptides for treatment of, e.g. arteriosclerosis and
 PT myoma -
 XX
 PS Claim 1; Page 76-80; 87pp; Japanese.
 XX
 CC This sequence is the human A55 protein of the invention. The protein
 CC can be used for the treatment of diseases due to abnormal proliferation
 CC of smooth muscle. The polypeptides can be used according their inhibition
 CC of the proliferation of vascular smooth muscle cells, particularly in
 CC treating arteriosclerosis or re-narrowing by vascular endothelial
 CC thickening after percutaneous transluminal coronary angioplasty (PTCA),
 CC or myoma, haematopoietic cell-regulatory activity, cytokine activity,
 CC tissue generation/reparation activity, actin/inhibin activity, taxis
 CC and chemotaxis activity, blood coagulation/thrombotic activity,
 CC receptor/ligand activity, cadherin/tumour metastasis inhibiting activity;
 CC tumour inhibition, and as a nutrient.
 XX
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2407; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.2e-159;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

| | | | |
|----|-----|--|-----|
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNCVDVDECATDSHQCNPTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNCVDVDECATDSHQCNPTQICI | 145 |
| Qy | 121 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 180 |
| | | | |
| Db | 146 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 205 |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 240 |
| | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | PGTYFCSCPPGYIILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQGGFKCIDPIRCEEPYL | 300 |
| | | | |
| Db | 266 | PGTYFCSCPPGYIILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQGGFKCIDPIRCEEPYL | 325 |
| Qy | 301 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 360 |
| | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 |
| | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 |
| Qy | 421 | YPF | 423 |
| | | | |
| Db | 446 | YPF | 448 |

RESULT 6

AAM93573

ID AAM93573 standard; Protein; 448 AA.

XX

AC AAM93573;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 3357.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-0114089.

XX

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2001-524255/58.
 DR N-PSDB; AAK94505.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 PS Claim 8; SEQ ID NO 3357; 1380pp + sequence listing; English.
 XX
 CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesising the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a polypeptide
 CC encoded by a full length human cDNA of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 XX
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2407; DB 22; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.2e-159;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS | 60 |
| | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS | 85 |
| Qy | 61 | TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICI | 145 |
| Qy | 121 | NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 180 |
| | | | |
| Db | 146 | NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 205 |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 240 |
| | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL | 300 |
| | | | |
| Db | 266 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL | 325 |
| Qy | 301 | RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 360 |
| | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 |
| | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 |

Qy 421 YPF 423
|||
Db 446 YPF 448

RESULT 7

AAU75494

ID AAU75494 standard; Protein; 448 AA.

XX

AC AAU75494;

XX

DT 23-APR-2002 (first entry)

XX

DE Human extracellular protein-like/EGF-like protein, EEGF.

XX

KW Human; extracellular protein-like protein; EGF-like;
KW protein; epidermal growth factor; EEGF; ATCC 97285; gene therapy;
KW vascular smooth muscle cell proliferation; Marfan syndrome;
KW wound healing; neurological trauma; acquired immunodeficiency syndrome;
KW AIDS-related dementia; ocular disorder; kidney disorder; liver disorder;
KW hair follicle growth promotion; burn; ulcer; corneal incision;
KW corneal inflammation; neoplasm; psoriasis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..25

FT /label= Signal_peptide

FT Protein 26..448

FT /label= Mature_EEGF

FT /note= "This region is specifically claimed in claim 10"

FT Domain 112..153

FT /label= EGF_1_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 154..190

FT /label= EGF_2_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 191..230

FT /label= EGF_3_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 231..271

FT /label= EGF_4_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 272..314

FT /label= EGF_5_domain

FT /note= "This domain is specifically claimed in claim 10"

XX

PN US2001051358-A1.

XX

PD 13-DEC-2001.

XX

PF 25-MAR-1999; 99US-0275805.

XX

PR 11-APR-1997; 97US-0839525.

PR 10-APR-1996; 96WO-US05247.

XX

PA (OLSE/) OLSEN H S.

Qy 301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
 |||
 Db 326 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy 361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
 |||
 Db 386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy 421 YPF 423
 |||
 Db 446 YPF 448

RESULT 8

AA08063

ID AA08063 standard; Protein; 448 AA.

XX

AC AA08063;

XX

DT 11-SEP-2000 (first entry)

XX

DE Human EGF-like homologue protein (PRO217) encoded by DNA32279 cDNA.

XX

KW Inflammatory cell infiltration; immune response; T cell proliferation;
 KW anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy;
 KW T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease;
 KW inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis;
 KW diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy;
 KW sclerosing cholangitis; inflammatory bowel disease; Whipple's disease;
 KW skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor;
 KW food hypersensitivity; urticaria; eosinophilic pneumonia; transplant;
 KW idiopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO217;
 KW EGF-like.

XX

OS Homo sapiens.

XX

PN WO9914241-A2.

XX

PD 25-MAR-1999.

XX

PF 17-SEP-1998; 98WO-US19437.

XX

PR 17-SEP-1997; 97US-0059119.

PR 18-SEP-1997; 97US-0059263.

PR 28-OCT-1997; 97US-0063550.

PR 12-NOV-1997; 97US-0065186.

PR 21-NOV-1997; 97US-0066364.

PR 24-NOV-1997; 97US-0066770.

PR 04-JUN-1998; 98US-0088026.

XX

PA (GETH) GENENTECH INC.

XX

PI Fong S, Goddard A, Gurney AL, Tumas D, Wood WI;

XX

DR WPI; 1999-229499/19.

DR N-PSDB; AAX37670.

XX

PT Composition containing novel polypeptide PRO245, its agonist or
PT antagonist -

XX

PS Example 1; Fig 6A; 177pp; English.

XX

CC This invention describes a novel composition containing (apart from a
CC carrier or excipient), a novel PRO245 polypeptide (I), its agonist or
CC antagonist, or their fragments, for modulating: (i) infiltration of
CC inflammatory cells into tissue; (ii) an immune response; or (iii) T cell
CC proliferation. The composition increases or decreases any of the effects
CC (i)-(iii). The products of the invention have anti-inflammatory,
CC anti-autoimmune and anti-diabetic activity. (I), and its (ant)agonists
CC and their fragments, are used to treat immune-related diseases,
CC particularly T cell-mediated diseases. The diseases treated include
CC systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic
CC arthritis, spondyloarthropathies, systemic sclerosis (scleroderma),
CC idiopathic inflammatory myopathies (dermatomyositis, polymyositis),
CC Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune
CC hemolytic anemia (immune pancytopenia, paroxysmal nocturnal
CC hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic
CC purpura immune-mediated thrombocytopenia), thyroiditis (Grave's disease,
CC Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic
CC thyroiditis), diabetes mellitus, immune-mediated renal disease
CC (glomerulonephritis, tubulointerstitial nephritis), multiple sclerosis,
CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic
CC inflammatory demyelinating polyneuropathy, infectious hepatitis
CC (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous
CC hepatitis, and sclerosing cholangitis, inflammatory bowel disease
CC (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and
CC Whipple's disease. Autoimmune or immune-mediated skin diseases including
CC bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis,
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
CC urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis,
CC hypersensitivity pneumonitis, and transplantation associated diseases
CC (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists
CC or fragment can also be used as an adjuvant in treatment of tumors.
CC Antibodies against (I) can also be used for diagnosing such diseases.
CC This sequence represents a human EGF-like homologue encoded by cDNA clone
CC DNA32279 which is described in the invention.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2401; DB 20; Length 448;
Best Local Similarity 99.8%; Pred. No. 3.2e-159;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCIPRTNPVYRGYPYNSPYS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCIPRTNPVYRGYPYNSPYS 85
Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHCNPTQICICI 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHCNPTQICICI 145
Qy 121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180

| | | | | | | | | | | |
|----|-----|--|------------|---------|----------|-------------|-----------|------------|----------|-------------------|
| Db | 146 | | NTGGYTCSC | TDGYW | LEGQCLDI | DECRYGYCQQL | CANVPGSYS | SCTCNPGFTL | NEDGRSC | 205 |
| Qy | 181 | | QDVNECATEN | PCVQTCV | NTYGSFI | CRCDPGYE | LEEDGVHC | SDMDECSF | SEFLCQHE | CVNQ 240 |
| Db | 206 | | QDVNECATEN | PCVQTCV | NTYGSFI | CRCDPGYE | LEEDGVHC | SDMDECSF | SEFLCQHE | CVNQ 265 |
| Qy | 241 | | PGTYFCSC | PPGYILL | DDNRSCQ | DINECEHR | NHTCNLQ | QTCYNLQ | GGFKCID | PIRCEEPYL 300 |
| Db | 266 | | PGTYFCSC | PPGYILL | DDNRSCQ | DINECEHR | NHTCNLQ | QTCYNLQ | GGFKCID | PIRCEEPYL 325 |
| Qy | 301 | | RISDNRCM | CPAENPG | CRDQPFT | ILYRDM | DVVSGR | SVPADIF | QMQATTR | YPGAYYIFQIKS 360 |
| Db | 326 | | RISDNRCM | CPAENPG | CRDQPFT | ILYRDM | DVVSGR | SVPADIF | QMQATTR | YPGAYYIFQIKS 385 |
| Qy | 361 | | GNEGREFY | MRQTGP | ISATLV | MTRPIK | GPRIQL | DLEMITV | NTVINFR | GSSVIRLRIYVSQ 420 |
| Db | 386 | | GNEGREFY | MRQTGP | ISATLV | MTRPIK | GPRIQL | DLEMITV | NTVINFR | GSSVIRLRIYVSQ 445 |
| Qy | 421 | | YPF | 423 | | | | | | |
| Db | 446 | | YPF | 448 | | | | | | |

RESULT 9

AAU29227

ID AAU29227 standard; Protein; 448 AA.

XX

AC AAU29227;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human PRO polypeptide sequence #204.

XX

KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200168848-A2.

XX

PD 20-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US06520.

XX

PR 01-MAR-2000; 2000WO-US05601.

PR 02-MAR-2000; 2000WO-US05841.

PR 03-MAR-2000; 2000US-187202P.

PR 06-MAR-2000; 2000US-186968P.

PR 14-MAR-2000; 2000US-189320P.

PR 14-MAR-2000; 2000US-189328P.

PR 15-MAR-2000; 2000WO-US06884.

PR 21-MAR-2000; 2000US-190828P.

PR 21-MAR-2000; 2000US-191007P.

PR 21-MAR-2000; 2000US-191048P.

PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2001-602746/68.

DR N-PSDB; AAS46128.

XX

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -

XX

PS Claim 11; Fig 408; 774pp; English.

XX

CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,

CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2401; DB 22; Length 448;
Best Local Similarity 99.8%; Pred. No. 3.2e-159;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 120
      |||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 145

Qy     121 NTEGGYTCSDTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||
Db     146 NTEGGYTCSDTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||
Db     206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      |||
Db     266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      |||
Db     326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||
Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
      |||
Db     446 YPF 448
```

RESULT 10

AAB31183

ID AAB31183 standard; Protein; 448 AA.

XX

AC AAB31183;

XX

DT 20-APR-2001 (first entry)

XX

DE Amino acid sequence of human polypeptide PRO210.

XX

KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;

KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;

KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;

KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;

KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
 KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /note= "signal peptide"
 FT Modified-site 21..27
 FT /note= "N-myristoylation site"
 FT Binding-site 54..57
 FT /note= "cell attachment site"
 FT Modified-site 64..70
 FT /note= "N-myristoylation site"
 FT Modified-site 144..156
 FT /note= "aspartic acid and asparagine hydroxylation site"
 FT Modified-site 149..155
 FT /note= "N-myristoylation site"
 FT Modified-site 186..192
 FT /note= "N-myristoylation site"
 FT Modified-site 226..232
 FT /note= "N-myristoylation site"
 FT Modified-site 242..248
 FT /note= "N-myristoylation site"
 FT Modified-site 267..273
 FT /note= "N-myristoylation site"
 FT Modified-site 283..287
 FT /note= "N-glycosylation site"
 FT Modified-site 296..300
 FT /note= "N-glycosylation site"
 FT Modified-site 310..316
 FT /note= "N-myristoylation site"
 XX
 PN WO200077037-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 22-MAY-2000; 2000WO-US14042.
 XX
 PR 15-JUN-1999; 99US-0139695.
 PR 20-JUL-1999; 99US-0145070.
 PR 26-JUL-1999; 99US-0145698.
 PR 17-AUG-1999; 99US-0149396.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28565.
 PR 07-DEC-1999; 99US-0169495.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.

PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;

XX

DR WPI; 2001-050091/06.

DR N-PSDB; AAC86968.

XX

PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides -

XX

PS Claim 12; Fig 10; 244pp; English.

XX

CC The present sequence represents a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2401; DB 22; Length 448;
Best Local Similarity 99.8%; Pred. No. 3.2e-159;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 60 |
| | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 85 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI | 145 |
| Qy | 121 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGF TLNEDGRSC | 180 |
| | | | |
| Db | 146 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGF TLNEDGRSC | 205 |

| | | | |
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| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 240 |
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| Db | 206 | QDVNECATENPCVQTCVNTYGLICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 300 |
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| Db | 266 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 325 |
| Qy | 301 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 360 |
| | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 |
| | | | |
| Db | 386 | GNEGREFYMRQTGPISATLMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 |
| Qy | 421 | YPF | 423 |
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| Db | 446 | YPF | 448 |

RESULT 11

ABU71315

ID ABU71315 standard; Protein; 448 AA.

XX

AC ABU71315;

XX

DT 10-JUN-2003 (first entry)

XX

DE Human PRO210 protein.

XX

KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
 KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
 KW differentiation; tumour; gene therapy.

XX

OS Homo sapiens.

XX

PN US2003036143-A1.

XX

PD 20-FEB-2003.

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PF 02-JUL-2002; 2002US-0187600.

XX

PR 16-SEP-1998; 98WO-US19330.

PR 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.

PR 08-MAR-1999; 99WO-US05028.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28551.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
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PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
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PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
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PR 01-APR-1998; 98US-080327P.
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| PR | 21-APR-1998; | 98US-082568P. |
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| PR | 22-APR-1998; | 98US-082797P. |
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| PR | 29-APR-1998; | 98US-083495P. |
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 PR 01-SEP-1998; 98US-098723P.
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 PR 02-SEP-1998; 98US-098821P.
 PR 02-SEP-1998; 98US-098843P.
 PR 09-SEP-1998; 98US-099602P.
 PR 10-SEP-1998; 98US-099741P.
 PR 10-SEP-1998; 98US-099754P.
 PR 10-SEP-1998; 98US-099763P.
 PR 10-SEP-1998; 98US-099812P.

Query Match 99.8%; Score 2401; DB 24; Length 448;
 Best Local Similarity 99.8%; Pred. No. 3.2e-159;
 Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 60 |
| | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 85 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI | 145 |
| Qy | 121 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 180 |
| | | | |
| Db | 146 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 205 |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 240 |
| | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 300 |
| | | | |
| Db | 266 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 325 |
| Qy | 301 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 360 |
| | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMIVNTVINFRGSSVIRLRIYVSQ | 420 |
| | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMIVNTVINFRGSSVIRLRIYVSQ | 445 |
| Qy | 421 | YPF | 423 |
| | | | |
| Db | 446 | YPF | 448 |

RESULT 12

ABU72040

ID ABU72040 standard; Protein; 448 AA.

XX

AC ABU72040;

XX

DT 11-JUN-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO210.

XX

KW Human; secreted and transmembrane polypeptide; PRO;

KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;

KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;

KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;

KW toxin; radiolabel; antibody; cell death; chromosome mapping;

KW gene mapping; transgenic animal; knockout animal; gene therapy;

KW tissue typing.

XX

OS Homo sapiens.

XX

PN US2002177165-A1.

XX

PD 28-NOV-2002.

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PF 01-FEB-2002; 2002US-0066500.
XX
PR 14-JUL-1998; 98WO-US14552.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 20-NOV-1998; 98WO-US24855.
PR 25-NOV-1998; 98WO-US25190.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 09-MAR-2000; 2000WO-US06471.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 26-AUG-1997; 97US-056974P.
PR 17-SEP-1997; 97US-059115P.
PR 18-SEP-1997; 97US-059263P.
PR 19-SEP-1997; 97US-059588P.
PR 17-OCT-1997; 97US-062285P.
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PR 27-OCT-1997; 97US-063329P.
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PR 25-NOV-1997; 97US-066840P.
PR 16-DEC-1997; 97US-069694P.
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PR 09-FEB-1998; 98US-074092P.
PR 25-MAR-1998; 98US-079294P.
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PR 26-JUL-1999; 99US-145698P.
PR 17-AUG-1999; 99US-149396P.
PR 07-DEC-1999; 99US-169495P.
PR 15-NOV-2001; 2001US-0002796.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;

XX

DR WPI; 2003-328482/31.

DR N-PSDB; ACA60458.

XX

PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, for identifying agonists
PT or antagonists of polypeptide, and as molecular weight markers -

XX

PS Claim 12; Fig 10; 254pp; English.

XX

CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337,
CC PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor
CC receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630,
CC PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a
CC cell expressing the above polypeptides. The bioactive molecule, a toxin,
CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
CC identify other proteins or molecules involved in binding interaction.
CC The polynucleotide (II) encoding (I) is useful in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, for generating
CC transgenic animals or knockout animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, to
CC construct hybridisation probes for mapping the gene which encodes the
CC PRO and for the genetic analysis of individuals with genetic disorders,
CC in gene therapy, for chromosome identification and as a chromosome
CC marker. (I) and (II) are useful for tissue typing. This is the amino
CC acid sequence of a novel human secreted and transmembrane PRO
CC polypeptide.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2401; DB 24; Length 448;
Best Local Similarity 99.8%; Pred. No. 3.2e-159;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
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Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHCNPTQICI 120
      |||
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Qy     121 NTEGGYTCSC TDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||
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      |||
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Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
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Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
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Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
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Db     446 YPF 448
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RESULT 13

ABU65772

ID ABU65772 standard; Protein; 448 AA.

XX

AC ABU65772;

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DT 19-MAY-2003 (first entry)

XX

DE Human secreted/transmembrane protein, SEQ ID 408.

XX

KW Human; PRO; secreted protein; transmembrane protein;

KW cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;

KW colon tumour; breast tumour; prostate tumour; rectal tumour;

KW cervical tumour; liver tumour; TNF-alpha release; arthritis;

KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;

KW cartilage disorder; sports injury.

XX

OS Homo sapiens.
XX
PN US2003036156-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188767.
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PR 16-SEP-1998; 98WO-US19330.
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AC      ABU66105;

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 KW Human; secreted protein; transmembrane protein; cytostatic;
 KW gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
 KW adrenal tumour; lung tumour; colon tumour; breast tumour;
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
 XX
 OS Homo sapiens.
 XX
 PN US2003036157-A1.
 XX
 PD 20-FEB-2003.
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 PF 02-JUL-2002; 2002US-0188769.
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 PR 16-SEP-1998; 98WO-US19330.
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 PR 14-MAY-1999; 99WO-US10733.
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 PR 02-DEC-1999; 99WO-US28551.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
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 PR 01-MAR-2000; 2000WO-US05601.
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RESULT 15

ABU67141

ID ABU67141 standard; Protein; 448 AA.

XX

AC ABU67141;

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DT 28-MAY-2003 (first entry)

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KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
KW PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tumour; obesity; diabetes; insulinaemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis.

XX

OS Homo sapiens.

XX

PN US2003032062-A1.

XX

PD 13-FEB-2003.

XX

PF 01-FEB-2002; 2002US-0066273.

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PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 26-AUG-1997; 97US-056974P.
PR 17-SEP-1997; 97US-059115P.
PR 18-SEP-1997; 97US-059263P.
PR 19-SEP-1997; 97US-059588P.
PR 17-OCT-1997; 97US-062285P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063082P.
PR 27-OCT-1997; 97US-063329P.
PR 29-OCT-1997; 97US-063733P.
PR 21-NOV-1997; 97US-066364P.
PR 25-NOV-1997; 97US-066840P.
PR 16-DEC-1997; 97US-069694P.
PR 09-FEB-1998; 98US-074086P.
PR 09-FEB-1998; 98US-074092P.
PR 25-MAR-1998; 98US-079294P.
PR 08-APR-1998; 98US-081049P.
PR 10-AUG-1998; 98US-095998P.
PR 18-AUG-1998; 98US-097000P.
PR 09-SEP-1998; 98US-099601P.
PR 10-SEP-1998; 98US-099803P.
PR 10-SEP-1998; 98US-099811P.
PR 10-SEP-1998; 98US-099812P.
PR 17-SEP-1998; 98US-100858P.
PR 24-SEP-1998; 98US-101922P.
PR 28-OCT-1998; 98US-106032P.
PR 20-NOV-1998; 98US-109304P.
PR 23-MAR-1999; 99US-125778P.
PR 15-JUN-1999; 99US-139695P.
PR 20-JUL-1999; 99US-145070P.
PR 26-JUL-1999; 99US-145698P.
PR 17-AUG-1999; 99US-149396P.
PR 07-DEC-1999; 99US-169495P.
PR 15-NOV-2001; 2001US-0002796.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;

XX

DR WPI; 2003-341963/32.

DR N-PSDB; ACA04448.

XX

PT New secreted and transmembrane polypeptide for modulating biological
PT activity of a cell expressing the polypeptide, identifying agonists or
PT antagonists of the polypeptide, and as molecular weight markers -

XX

PS Claim 12; Fig 10; 254pp; English.

XX

CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptides. The bioactive molecule causes cell
CC death. (II) Is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ab is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or
CC anti-PRO antibody e.g. a tumour. (I) is useful for treating obesity,
CC diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency
CC disorders, for inhibiting tumour growth, enhances vascular permeability
CC and immune response, for inducing regeneration of auditory hair cells and
CC for treating hearing loss in mammals, and for treating bone and/or
CC cartilage disorders such as sports injuries and arthritis. This is the
CC amino acid sequence of a novel human secreted and transmembrane
CC polypeptide.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2401; DB 24; Length 448;
Best Local Similarity 99.8%; Pred. No. 3.2e-159;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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| Qy | 61 | TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI | 145 |
| Qy | 121 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 180 |
| | | | |
| Db | 146 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 205 |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQ | 240 |

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|----|-----|--|--|--|--------------------------------------|-----|
| Db | 206 | | QDVNECATENPCVQTCVNTYGS | | CRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | | | 300 |
| Db | 266 | | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | | | 325 |
| Qy | 301 | | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | | | 360 |
| Db | 326 | | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | | | 385 |
| Qy | 361 | | GNEGREFYMRQTGPISATLMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | | | 420 |
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| Db | 446 | | YPF | | 448 | |

Search completed: January 9, 2004, 12:33:34
Job time : 38.3949 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2004, 12:30:17 ; Search time 15.0551 Seconds
(without alignments)
1188.799 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|--------|---------|--------|----|--------------------|-------------------|
| | | Match | Length | | | |
| 1 | 2407 | 100.0 | 448 | 2 | US-08-884-072-1 | Sequence 1, Appli |
| 2 | 2407 | 100.0 | 448 | 4 | US-09-212-168-1 | Sequence 1, Appli |
| 3 | 1827 | 75.9 | 335 | 4 | US-09-312-283C-186 | Sequence 186, App |
| 4 | 1791 | 74.4 | 337 | 3 | US-09-188-930-186 | Sequence 186, App |
| 5 | 1276.5 | 53.0 | 443 | 2 | US-08-833-963C-2 | Sequence 2, Appli |
| 6 | 1276.5 | 53.0 | 443 | 3 | US-08-980-514-1 | Sequence 1, Appli |
| 7 | 963.5 | 40.0 | 387 | 2 | US-08-884-072-5 | Sequence 5, Appli |
| 8 | 963.5 | 40.0 | 387 | 2 | US-08-833-963C-9 | Sequence 9, Appli |
| 9 | 963.5 | 40.0 | 387 | 3 | US-08-980-514-3 | Sequence 3, Appli |
| 10 | 963.5 | 40.0 | 387 | 4 | US-09-212-168-5 | Sequence 5, Appli |
| 11 | 912.5 | 37.9 | 274 | 3 | US-09-188-930-336 | Sequence 336, App |

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| 12 | 912.5 | 37.9 | 274 | 4 | US-09-312-283C-336 | Sequence 336, App |
| 13 | 539 | 22.4 | 1394 | 6 | 5177197-30 | Patent No. 5177197 |
| 14 | 518 | 21.5 | 575 | 4 | US-09-482-273-159 | Sequence 159, App |
| 15 | 518 | 21.5 | 638 | 4 | US-09-482-273-245 | Sequence 245, App |
| 16 | 455 | 18.9 | 638 | 2 | US-08-897-443-1 | Sequence 1, Appli |
| 17 | 453 | 18.8 | 1833 | 3 | US-08-479-722B-2 | Sequence 2, Appli |
| 18 | 453 | 18.8 | 1833 | 5 | PCT-US95-02251-18 | Sequence 18, Appl |
| 19 | 438 | 18.2 | 1251 | 5 | PCT-US95-02251-3 | Sequence 3, Appli |
| 20 | 438 | 18.2 | 1252 | 1 | US-08-199-780-3 | Sequence 3, Appli |
| 21 | 438 | 18.2 | 1252 | 2 | US-08-316-650-3 | Sequence 3, Appli |
| 22 | 438 | 18.2 | 1253 | 3 | US-08-479-722B-4 | Sequence 4, Appli |
| 23 | 431 | 17.9 | 956 | 2 | US-08-897-443-3 | Sequence 3, Appli |
| 24 | 392 | 16.3 | 886 | 3 | US-09-110-116-3 | Sequence 3, Appli |
| 25 | 389.5 | 16.2 | 353 | 4 | US-09-482-273-243 | Sequence 243, App |
| 26 | 372 | 15.5 | 810 | 2 | US-08-820-170A-34 | Sequence 34, Appl |
| 27 | 372 | 15.5 | 810 | 3 | US-09-055-699-34 | Sequence 34, Appl |
| 28 | 372 | 15.5 | 810 | 3 | US-09-273-565-34 | Sequence 34, Appl |
| 29 | 372 | 15.5 | 810 | 4 | US-09-565-538-34 | Sequence 34, Appl |
| 30 | 372 | 15.5 | 810 | 4 | US-09-661-468-34 | Sequence 34, Appl |
| 31 | 372 | 15.5 | 810 | 4 | US-09-976-165-34 | Sequence 34, Appl |
| 32 | 369 | 15.3 | 2471 | 1 | US-08-185-432-16 | Sequence 16, Appl |
| 33 | 369 | 15.3 | 2471 | 1 | US-08-083-590A-19 | Sequence 19, Appl |
| 34 | 369 | 15.3 | 2471 | 3 | US-08-532-384-19 | Sequence 19, Appl |
| 35 | 369 | 15.3 | 2471 | 4 | US-08-899-232-1 | Sequence 1, Appli |
| 36 | 361.5 | 15.0 | 816 | 2 | US-08-820-170A-37 | Sequence 37, Appl |
| 37 | 361.5 | 15.0 | 816 | 3 | US-09-055-699-37 | Sequence 37, Appl |
| 38 | 361.5 | 15.0 | 816 | 3 | US-09-273-565-37 | Sequence 37, Appl |
| 39 | 361.5 | 15.0 | 816 | 4 | US-09-565-538-37 | Sequence 37, Appl |
| 40 | 361.5 | 15.0 | 816 | 4 | US-09-661-468-37 | Sequence 37, Appl |
| 41 | 361.5 | 15.0 | 816 | 4 | US-09-976-165-37 | Sequence 37, Appl |
| 42 | 354.5 | 14.7 | 1964 | 4 | US-09-467-997-1 | Sequence 1, Appli |
| 43 | 351.5 | 14.6 | 2703 | 1 | US-08-185-432-19 | Sequence 19, Appl |
| 44 | 351.5 | 14.6 | 2703 | 4 | US-08-899-232-4 | Sequence 4, Appli |
| 45 | 350.5 | 14.6 | 652 | 2 | US-08-751-305-2 | Sequence 2, Appli |

ALIGNMENTS

RESULT 1

US-08-884-072-1

; Sequence 1, Application US/08884072

; Patent No. 5872234

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,072
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CORNNOT01
; CLONE: 45517
US-08-884-072-1

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Query Match          100.0%; Score 2407; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.7e-182;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPQTQICI 120
      |||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPQTQICI 145

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      |||
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 Db 446 YPF 448

RESULT 2

US-09-212-168-1

; Sequence 1, Application US/09212168

; Patent No. 6303765

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/212,168

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/884,072

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0333 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 448 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: CORNNOT01

; CLONE: 45517

US-09-212-168-1

Query Match 100.0%; Score 2407; DB 4; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.7e-182;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
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Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy     61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPTQICI 120
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Db     86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPTQICI 145

Qy    121 NTEGGYTCSCCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
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Qy    241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 300
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RESULT 3
 US-09-312-283C-186
 ; Sequence 186, Application US/09312283C
 ; Patent No. 6573095
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells
 ; TITLE OF INVENTION: and Methods for Their Use
 ; FILE REFERENCE: 11000.1011c2
 ; CURRENT APPLICATION NUMBER: US/09/312,283C
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 425
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 186


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; LOCATION: (141)...(141)
; NAME/KEY: UNSURE
; LOCATION: (166)...(166)
; NAME/KEY: UNSURE
; LOCATION: (167)...(167)
; NAME/KEY: UNSURE
; LOCATION: (183)...(183)
US-09-188-930-186

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Query Match          74.4%;  Score 1791;  DB 3;  Length 337;
Best Local Similarity 93.7%;  Pred. No. 5.4e-134;
Matches 314;  Conservative 6;  Mismatches 15;  Indels 0;  Gaps 0;

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Qy     269 HRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDM 328
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Db     243 DVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 302

Qy     389 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
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Db     303 RDIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 337

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RESULT 5

US-08-833-963C-2

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; Sequence 2, Application US/08833963C
; Patent No. 5916769
; GENERAL INFORMATION:
; APPLICANT: Olsen, et al.
; TITLE OF INVENTION: Extracellular/Epidermal Growth Factor
; TITLE OF INVENTION: HCABA58X
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: USA

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; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS.
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,963C
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/05033
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF258
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-963C-2

```

```

Query Match          53.0%; Score 1276.5; DB 2; Length 443;
Best Local Similarity 52.0%; Pred. No. 3.1e-93;
Matches 220; Conservative 67; Mismatches 119; Indels 17; Gaps 4;

```

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      :||:|::| | | |::|| |||||:|:| |:| |||||:|:| | :
Db      38 ECTDGYEWDPDPSQHCRDVNECLTIPEACKGEMKCINHYGGYLCLPRSAAVINDLHG---- 93

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICICI 120
      || | || || | | | | | | | | | | | | | | | | | | | | | | | |
Db      94 ---EGP-PPVPVPAQHPN-----PCPPGYEPDDQDSCVDVDECAQALHDCRPSQDCH 141

Qy      121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      | | | |:| || | : :|:||||||| || | | |:|:| | | | | | | | : |||
Db      142 NLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSC 201

Qy      181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      ||||| || | | |:|:|:|:| || | | | | | | | | | | | | | | | |
Db      202 VDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSSYSSYLCQYRCVNE 261

Qy      241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      || : | || | | | | | | | | | | | | | | | | | | | | | | | | |
Db      262 PGRFSCHCPQGYQLL-ATRLCQDIDECESGAHQCSAQTCVNFHGGYRCVDTNRCVEPYI 320

Qy      301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      :|:|:|:|:| | | | |:|:| | | : | | | | | | | | | | | | | | | |
Db      321 QVSENRLCPASNPLCREQPSSIVHRYMTITERSVPADVFIQATSVPYPGAYNAFQIRA 380

Qy      361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420

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      || :||:| | :|| ||: ||: |||| |||||:|:|:::| |||:| | :|
Db      381 GNSQGDFYIRQINNVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGA 440

QY      421 YPF 423
      | |
Db      441 YTF 443

```

RESULT 6

US-08-980-514-1

```

; Sequence 1, Application US/08980514
; Patent No. 6004753
; GENERAL INFORMATION:
;   APPLICANT: Yue, Henry
;   APPLICANT: Guegler, Karl J.
;   APPLICANT: Shah, Purvi
;   TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT
;   TITLE OF INVENTION: EIN
;   NUMBER OF SEQUENCES: 3
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Dr.
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/980,514
;     FILING DATE: Filed Herewith
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PF-0436 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-855-0555
;     TELEFAX: 650-845-4166
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 443 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     IMMEDIATE SOURCE:
;       LIBRARY: BRSTNOT13
;       CLONE: 2786449

```

US-08-980-514-1

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Query Match          53.0%; Score 1276.5; DB 3; Length 443;
Best Local Similarity 52.0%; Pred. No. 3.1e-93;

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Matches 220; Conservative 67; Mismatches 119; Indels 17; Gaps 4;

RESULT 7

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,072
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458228
US-08-884-072-5

```

```

Query Match          40.0%; Score 963.5; DB 2; Length 387;
Best Local Similarity 48.3%; Pred. No. 1.4e-68;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```

```

Qy      71 APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSC 130
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 189
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCSPGFQLAANNYTCVDINECDAS 155

Qy     190 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCP 249
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy     250 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPLYRISDNRCMC 309
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPENRCVC 273

Qy     310 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 369
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     274 PVSNAMECRELPQSIVYKYSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFY 333

Qy     370 RQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRFTSSVLRRLTIIVGPFSF 387

```

RESULT 8
 US-08-833-963C-9

; Sequence 9, Application US/08833963C
 ; Patent No. 5916769
 ; GENERAL INFORMATION:
 ; APPLICANT: Olsen, et al.
 ; TITLE OF INVENTION: Extracellular/Epidermal Growth Factor
 ; TITLE OF INVENTION: HCABA58X
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Ave
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,963C
 ; FILING DATE: 11-APR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US96/05033
 ; FILING DATE: 10-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF258
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8439
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 387 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-833-963C-9

Query Match 40.0%; Score 963.5; DB 2; Length 387;
 Best Local Similarity 48.3%; Pred. No. 1.4e-68;
 Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

| | | | |
|----|-----|--|-----|
| Qy | 71 | APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNP | 130 |
| | | : : : : : : | |
| Db | 38 | ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC | 95 |
| Qy | 131 | TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE | 189 |
| | | : : : | |
| Db | 96 | PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCVDINECDAS | 155 |
| Qy | 190 | NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCP | 249 |
| | | : : : : : : | |
| Db | 156 | NQCAQQCYNILGSFICQCNQGYELSSDRLNCEIDECRTSSYLCQYQCVNEPGKFSCMCP | 215 |

Qy 250 PGYIILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC 309
 || :: :|:||||||| | | : |:| |||:| |:| |:| :|:|:
 Db 216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPEINRCVC 273
 Qy 310 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 369
 | | ||: | :|:|: | : | |||:||||:|||| | |:||||| |||:
 Db 274 PVSNAMECRELPQSIVYKYSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYL 333
 Qy 370 RQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
 ||| |:| ||: : : |||| :|||:|:|:| || |||:| | | : |
 Db 334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFTTSSVLRLTIIVGPFSF 387

RESULT 9

US-08-980-514-3

; Sequence 3, Application US/08980514
 ; Patent No. 6004753
 ; GENERAL INFORMATION:
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT
 ; TITLE OF INVENTION: EIN
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/980,514
 ; FILING DATE: Filed Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0436 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 387 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:

; LIBRARY: GenBank
; CLONE: 458228
US-08-980-514-3

Query Match 40.0%; Score 963.5; DB 3; Length 387;
Best Local Similarity 48.3%; Pred. No. 1.4e-68;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```
Qy      71 APPLSAPNYPTISRPLICRFGYQMDESNCVDVDECATDSHQCNPQTQICINTEGGYTCSC 130
      | | | | : | | : | | : | | : | | : | | : | | : | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 189
      | | | | : | | | | | | | | : | | : | | : | | : | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCSPGFLAANNYTCTVDINECDAS 155

Qy     190 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPQGTFCSCP 249
      | | | | | | | | : | | | | | : | | : | | : | | : | |
Db     156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy     250 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEYPYLRISDNRCMC 309
      | | : : : | | | | | | | | | : | : | | | | : | | : | |
Db     216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPEINRCVC 273

Qy     310 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 369
      | | | | : | : | : | : | | | | : | | | | | | | | : | |
Db     274 PVSNAMECRELPQSIVYKYSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYL 333.

Qy     370 RQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | : | | | : : : | | | : | | | : | | : | | : | |
Db     334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 387
```

RESULT 10

US-09-212-168-5

; Sequence 5, Application US/09212168

; Patent No. 6303765

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/212,168

```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/884,072
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458228
US-09-212-168-5

```

```

Query Match          40.0%; Score 963.5; DB 4; Length 387;
Best Local Similarity 48.3%; Pred. No. 1.4e-68;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```

```

Qy      71 APPLSAPNYPTISRPLICRFGYQMDESNQVDVDECATDSHCNPTQICINTEGGYTCSC 130
      | | | | : | | : | | | | : | | | : | | | : | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCNPGFTLNEDGRSCQDVNECATE 189
      | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQSPGFQLAANNYTCDINECDAS 155

Qy     190 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCP 249
      | | | | | | | | | | | | | | | | | | | | | |
Db     156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy     250 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEYPYLRISDNRCMC 309
      | | : : : | | | | | | | | | | | | | | | | |
Db     216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPENRCVC 273

Qy     310 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 369
      | | | | | : | : | : | : | | | | | | | | | |
Db     274 PVSNAMECRELPQSIVYKYSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGFEFYL 333

Qy     370 RQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | : | | | : : | | | | : | | | | : | |
Db     334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSS 387

```

```

RESULT 11
US-09-188-930-336
; Sequence 336, Application US/09188930A
; Patent No. 6150502

```

```
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 336
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-336
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Query Match          37.9%; Score 912.5; DB 3; Length 274;
Best Local Similarity 56.0%; Pred. No. 1e-64;
Matches 154; Conservative 47; Mismatches 73; Indels 1; Gaps 1;
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Qy      149 YGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 208
      | | | | | | : | | | | | : | | | | | | | | | | | | : | | | | | |
Db      1 YRYCQHRCVNLPGSFRCQCEPGFQLGPNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCH 60

Qy      209 PGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 268
      | | | | | | | | | | | | : | | | | | | : | | | | | | | | | | | |
Db      61 QGYELHRDGFSCSDIDECSYSSYLCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECE 119

Qy      269 HRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDM 328
      | | : | | | | | | | | | | | | : | | | | | | : | | | | | | : | | |
Db      120 SGAHQCSEAQTCVNFHGGYRCVDTNRCVEPYIQVSENRCLCPASNPLCREQPSSIVHRYM 179

Qy      329 DVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 388
      : | | | | | | : | | | | | | | | | | | | : | | | | : | | | | | |
Db      180 TITSERVSPADV FQIQATSVYPGAYNAFQIRAGNSQGDFYIRQINNVSAMLVLARPVTPG 239

Qy      389 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | | | : | | | | | | | | | | | | : | | | |
Db      240 REYVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF 274
```

RESULT 12

US-09-312-283C-336

```
; Sequence 336, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
```

; FILE REFERENCE: 11000.1011c2
 ; CURRENT APPLICATION NUMBER: US/09/312,283C
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 425
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 336
 ; LENGTH: 274
 ; TYPE: PRT
 ; ORGANISM: Mouse
 US-09-312-283C-336

Query Match 37.9%; Score 912.5; DB 4; Length 274;
 Best Local Similarity 56.0%; Pred. No. 1e-64;
 Matches 154; Conservative 47; Mismatches 73; Indels 1; Gaps 1;

Qy 149 YGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 208
 | ||| | :|||: | | ||| | : ||| |||| | | | | :|||:| |||
 Db 1 YRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCH 60
 Qy 209 PGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 268
 |||| | | |||:||||:| :|||: |||:| | : | | | | | | | | ||||:| |||
 Db 61 QGYELHRDGFSCSDIDECSSYSSYLCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECE 119
 Qy 269 HRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDM 328
 | : | || | | ||:|:| | | |||:|:| |||:| || | | | | :|:| | |
 Db 120 SGAHQCEAQTCTVNFHGGYRCVDTNRCVEPYIQVSENRLCPASNPLCREQPSSIVHRYM 179
 Qy 329 DVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 388
 : | |||||:|:|:|:| |||| | |||:| | :|:| | :| | | :|:| |
 Db 180 TITSERVSPADV FQIQATSVYPGAYNAFQIRAGNSQGDFYIRQINNVSAMLVLARVPTGP 239
 Qy 389 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
 || |||||:|:|:|:| |||:| | :| | |
 Db 240 REYVLDLEMTMNSLSMSYRASSVLRLTVFVGAYTF 274

RESULT 13
 5177197-30
 ;Patent No. 5177197
 ; APPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
 ;WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
 ;LENA;HELDIN, CARL-HENRIK
 ; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
 ;HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
 ; NUMBER OF SEQUENCES: 53
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/487,343
 ; FILING DATE: 27-FEB-1990
 ;SEQ ID NO:30:
 ; LENGTH: 1394
 5177197-30

Query Match 22.4%; Score 539; DB 6; Length 1394;
 Best Local Similarity 29.6%; Pred. No. 1.9e-34;
 Matches 126; Conservative 51; Mismatches 126; Indels 122; Gaps 17;

Qy 2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYST 61

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| Db | 573 | CYEGYRFSEQQRKCVDIDECTQVQHLC-SQGRCENTEGSF LCI----- | 614 |
| Qy | 62 | PYSGPYPAAPPLSAPNYPTISRPLI-----CRFGYQMDASNQCVDVD | 104 |
| Db | 615 | -CPAGFMASEEGTNCIDVDECLRPDVCGEHCVNTVGAFRCEYCDSGYRMTQRGRCEDID | 673 |
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| Db | 674 | ECLNPS-TC-PDEQCVNSPGSYQCVPTTEGFRGWNGQCLDVDECLPNVCANGDCSNLEG | 731 |
| Qy | 162 | SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQ----- | 194 |
| Db | 732 | SYMCSCHKGYTRTPDHKHCARDIDECQGNLCVNGQCKNTEGSFRCTCGQGYQLSAAKDQC | 791 |
| Qy | 195 | -----TCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQH-ECV | 238 |
| Db | 792 | EDIDECQHRHLCAHGQCRNTEGSFQCVCDQGYRASGLGDHCEINEDKESVCQRGDCI | 851 |
| Qy | 239 | NQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCI----- | 290 |
| Db | 852 | NTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEGSFHCVCQQGFSIS | 909 |
| Qy | 291 | -DPIRCEEPYLRIS-----DN-----RCMC-----PAENPGCRDQPFTILYRDM | 328 |
| Db | 910 | ADGRTCEDIDECVNNTVCDSHGFCDNTAGSFRCCLCYQGFQAPQDGQGCVD-----VNEC | 963 |
| Qy | 329 | DVMSG 333 | |
| Db | 964 | ELLSG 968 | |

RESULT 14

US-09-482-273-159

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; Sequence 159, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: PZ030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 159
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-159

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Query Match 21.5%; Score 518; DB 4; Length 575;
 Best Local Similarity 29.5%; Pred. No. 3.2e-33;
 Matches 140; Conservative 56; Mismatches 157; Indels 122; Gaps 20;

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Db      170 CPEGFELDSQGAFCVDVDECAWDAHLCREGQRCVNLLGSYRCLPDCGP----- 217

Qy      62 PYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICIN 121
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Db      218 -----GFRVADGAGCEDVDECLEGLDDCHYNQLCEN 248

Qy     122 TEGGYTCSTDGWLLLEG---QCLDIDECRY--GYCQQLCANVPGSYSCTCNPGFTLNED 176
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Qy     177 GRSC-----QDVNECATENPCV-----QTCVNTYGSFI-----CRCD 208
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Db     368 PGF-IRQNGV-CTDLDECRVRN-LCQHACRNTEGSYQCLCPAGYRLLPSGKNCQDINECE 424

Qy     269 HRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPA-----ENPG-----CRD 318
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Db     425 EESIECGPGQMCFNTRGSYQCVD-----TPCPATYRQGPSPGTCFRRCSQ 469

Qy     319 Q-----PFTILYRDMDVVSGRSVPADIFQMQATTR--YPGAYYIFQIKSGNEGREFYMRQ 371
      | | : | | : : | | : : | : | : : | : | : | : |
Db     470 DCGTGGPSTLQYRLLPLPLGVRAHHDVARLTAFSEVGVPANRTELSMLEPDRSPFALR- 528

Qy     372 TGPISATL--VMTRPIKGPRI-QLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
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RESULT 15

US-09-482-273-245

; Sequence 245, Application US/09482273

; Patent No. 6534631

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 71 Human Secreted Proteins

; FILE REFERENCE: PZ030P1

; CURRENT APPLICATION NUMBER: US/09/482,273

; CURRENT FILING DATE: 2000-01-13

; EARLIER APPLICATION NUMBER: PCT/US99/15849

; EARLIER FILING DATE: 1999-07-14

; EARLIER APPLICATION NUMBER: 60/092,921

; EARLIER FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: 60/092,922

; EARLIER FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: 60/092,956

; EARLIER FILING DATE: 1998-07-15

; NUMBER OF SEQ ID NOS: 267

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-245

Query Match 21.5%; Score 518; DB 4; Length 638;
Best Local Similarity 29.5%; Pred. No. 3.6e-33;
Matches 140; Conservative 56; Mismatches 157; Indels 122; Gaps 20;

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Db      233 CPEGFELDSQGAFCVDVDECAWDAHLCREGQRCVNLLGSYRCLPDCGP----- 280

Qy      62 PYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICIN 121
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Qy     122 TEGGYTCSDTDGYWLLEG---QCLDIDECRY--GYCQQLCANVPGSYSCTCNPGFTLNED 176
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Qy     177 GRSC-----QDVNECATENPCV-----QTCVNTYGSFI-----CRCD 208
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      : | | | | : | : | : | : | : | | | | | | | | | |
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Qy     319 Q-----PFTILYRDMDVVSGRSVPADIFQM QATTR--YPGAYYIFQIKSGNEGREFYMRQ 371
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Job time : 16.0551 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:34:12 ; Search time 28.1676 Seconds
(without alignments)
3026.121 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % | Query | | | | | |
|--------|-------|--------------|----|----|--|--|-------------|
| No. | Score | Match Length | DB | ID | | | Description |

| | | | | | | |
|----|------|-------|-----|----|-------------------|-------------------|
| 1 | 2407 | 100.0 | 448 | 9 | US-09-083-002-2 | Sequence 2, Appli |
| 2 | 2407 | 100.0 | 448 | 9 | US-09-275-805-2 | Sequence 2, Appli |
| 3 | 2407 | 100.0 | 448 | 9 | US-09-836-561-1 | Sequence 1, Appli |
| 4 | 2407 | 100.0 | 448 | 14 | US-10-041-016-2 | Sequence 2, Appli |
| 5 | 2401 | 99.8 | 448 | 12 | US-10-199-672-408 | Sequence 408, App |
| 6 | 2401 | 99.8 | 448 | 12 | US-10-187-749-408 | Sequence 408, App |
| 7 | 2401 | 99.8 | 448 | 12 | US-10-194-457-408 | Sequence 408, App |
| 8 | 2401 | 99.8 | 448 | 12 | US-10-184-642-408 | Sequence 408, App |
| 9 | 2401 | 99.8 | 448 | 12 | US-10-196-747-408 | Sequence 408, App |
| 10 | 2401 | 99.8 | 448 | 12 | US-10-173-689-408 | Sequence 408, App |
| 11 | 2401 | 99.8 | 448 | 12 | US-10-173-690-408 | Sequence 408, App |
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| 16 | 2401 | 99.8 | 448 | 12 | US-10-173-699-408 | Sequence 408, App |
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| 19 | 2401 | 99.8 | 448 | 12 | US-10-174-583-408 | Sequence 408, App |
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| 22 | 2401 | 99.8 | 448 | 12 | US-10-174-591-408 | Sequence 408, App |
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| 24 | 2401 | 99.8 | 448 | 12 | US-10-175-742-408 | Sequence 408, App |
| 25 | 2401 | 99.8 | 448 | 12 | US-10-175-744-408 | Sequence 408, App |
| 26 | 2401 | 99.8 | 448 | 12 | US-10-175-745-408 | Sequence 408, App |
| 27 | 2401 | 99.8 | 448 | 12 | US-10-175-748-408 | Sequence 408, App |
| 28 | 2401 | 99.8 | 448 | 12 | US-10-175-751-408 | Sequence 408, App |
| 29 | 2401 | 99.8 | 448 | 12 | US-10-175-754-408 | Sequence 408, App |
| 30 | 2401 | 99.8 | 448 | 12 | US-10-176-480-408 | Sequence 408, App |
| 31 | 2401 | 99.8 | 448 | 12 | US-10-176-489-408 | Sequence 408, App |
| 32 | 2401 | 99.8 | 448 | 12 | US-10-176-754-408 | Sequence 408, App |
| 33 | 2401 | 99.8 | 448 | 12 | US-10-176-755-408 | Sequence 408, App |
| 34 | 2401 | 99.8 | 448 | 12 | US-10-176-759-408 | Sequence 408, App |
| 35 | 2401 | 99.8 | 448 | 12 | US-10-176-920-408 | Sequence 408, App |
| 36 | 2401 | 99.8 | 448 | 12 | US-10-176-922-408 | Sequence 408, App |
| 37 | 2401 | 99.8 | 448 | 12 | US-10-176-924-408 | Sequence 408, App |
| 38 | 2401 | 99.8 | 448 | 12 | US-10-176-984-408 | Sequence 408, App |
| 39 | 2401 | 99.8 | 448 | 12 | US-10-179-508-408 | Sequence 408, App |
| 40 | 2401 | 99.8 | 448 | 12 | US-10-179-512-408 | Sequence 408, App |
| 41 | 2401 | 99.8 | 448 | 12 | US-10-179-515-408 | Sequence 408, App |
| 42 | 2401 | 99.8 | 448 | 12 | US-10-066-198-15 | Sequence 15, Appl |
| 43 | 2401 | 99.8 | 448 | 12 | US-10-173-702-408 | Sequence 408, App |
| 44 | 2401 | 99.8 | 448 | 12 | US-10-173-703-408 | Sequence 408, App |
| 45 | 2401 | 99.8 | 448 | 12 | US-10-173-704-408 | Sequence 408, App |

ALIGNMENTS

RESULT 1

US-09-083-002-2

; Sequence 2, Application US/09083002

; Patent No. US20010016650A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

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; APPLICANT: McCoy, John M.
; APPLICANT: Racie, Lisa A.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Evans, Cheryl
; APPLICANT: Agostino, Michael
; APPLICANT: Lu, Zhijian
; APPLICANT: Honjo, Tasuku
; APPLICANT: Tashiro, Kei
; APPLICANT: Nakamura, Tomoyuki
; TITLE OF INVENTION: SECRETED PROTEINS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,002
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-083-002-2

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Query Match          100.0%; Score 2407; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.3e-183;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85
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Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHCNPTQICI 120
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Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHCNPTQICI 145
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| Db | 146 | | NTGGYTCSC | TDGYWLL | EGQCLDI | DECRYGYC | QQLCANV | PGSYSCTC | NPFGFTL | NEDGRSC | 205 | |
| Qy | 181 | | QDVNECAT | ENPCVQT | CVNTYGS | FI | CRCDPGY | ELEEDGV | HCSMD | DECSFSE | FLCQHECVNQ | 240 |
| Db | 206 | | QDVNECAT | ENPCVQT | CVNTYGS | FI | CRCDPGY | ELEEDGV | HCSMD | DECSFSE | FLCQHECVNQ | 265 |
| Qy | 241 | | PGTYFCSC | PPGYILL | DDNRSCQ | DINECEH | RNHTCN | LQQT | CYNLQ | GGFKC | IDPIRCEEPYL | 300 |
| Db | 266 | | PGTYFCSC | PPGYILL | DDNRSCQ | DINECEH | RNHTCN | LQQT | CYNLQ | GGFKC | IDPIRCEEPYL | 325 |
| Qy | 301 | | RISDNRCM | CPAENP | GCRDQ | PFTILYR | DMVVS | GRSVP | ADIFQ | MQATTRY | PGAYYIFQIKS | 360 |
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| Qy | 421 | | YPF | 423 | | | | | | | | |
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RESULT 2

US-09-275-805-2

; Sequence 2, Application US/09275805

; Patent No. US20010051358A1

; GENERAL INFORMATION:

; APPLICANT: OLSEN, HENRIK S.

; APPLICANT: LI, HAODONG

; TITLE OF INVENTION: EXTRACELLULAR EPIDERMAL GROWTH FACTOR

; TITLE OF INVENTION: LIKE PROTEIN

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: US

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/275,805

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/839,525

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: BROOKES, ANDERS A.

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PF224

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8509
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-275-805-2

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Query Match          100.0%; Score 2407; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.3e-183;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

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      |||
Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
      |||
Db     446 YPF 448

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RESULT 3

US-09-836-561-1

; Sequence 1, Application US/09836561

; Patent No. US20020038006A1

GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; Corley, Neil C.

; Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

```

; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/836,561
;   FILING DATE: 16-Apr-2001
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/212,168
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 448 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: CORNNOT01
;   CLONE: 45517
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-836-561-1

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Query Match          100.0%;  Score 2407;  DB 9;  Length 448;
Best Local Similarity 100.0%;  Pred. No. 3.3e-183;
Matches 423;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy     61 TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     86 TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 145

Qy    121 NTEGGYTCSTDGWYLLLEGQCLDIDECRYGYCQQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    146 NTEGGYTCSTDGWYLLLEGQCLDIDECRYGYCQQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy    181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQ 240

```

| | | | | |
|----|-----|-----|---|-----|
| Db | 206 | | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL | 300 |
| Db | 266 | | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL | 325 |
| Qy | 301 | | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 360 |
| Db | 326 | | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 |
| Db | 386 | | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 |
| Qy | 421 | YPF | 423 | |
| Db | 446 | YPF | 448 | |

RESULT 4

US-10-041-016-2

; Sequence 2, Application US/10041016

; Publication No. US20020165151A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Racie, Lisa A.
; LaVallie, Edward R.
; Merberg, David
; Treacy, Maurice
; Evans, Cheryl
; Agostino, Michael
; Lu, Zhijian
; Honjo, Tasuku

; TITLE OF INVENTION: SECRETED PROTEINS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/041,016
; FILING DATE: 07-Jan-2002
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/083,002
; FILING DATE: 21-MAR-1998

; ATTORNEY/AGENT INFORMATION:


```

;      NAME: Sprunger, Suzanne A.
;      REGISTRATION NUMBER: P-41,323
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (617) 498-8284
;      TELEFAX: (617) 876-5851
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 448 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: No. US20020165151A1 Relevant
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-041-016-2

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Query Match          100.0%;  Score 2407;  DB 14;  Length 448;
Best Local Similarity 100.0%;  Pred. No. 3.3e-183;
Matches 423;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

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Qy      1  QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26  QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 85

Qy      61  TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      86  TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI 145

Qy     121  NTEGGYTCSTDGWYLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     146  NTEGGYTCSTDGWYLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181  QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     206  QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241  PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     266  PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301  RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     326  RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy     361  GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     386  GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421  YPF 423
      |||
Db     446  YPF 448

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RESULT 5
US-10-199-672-408
; Sequence 408, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:

```

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-408

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Query Match          99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
         |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85
         |||
Qy      61 TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 120
         |||
Db      86 TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 145
         |||
Qy     121 NTEGGYTCSCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180

```

| | | | | | | | | | | | | | |
|----|-----|--|-----------|---------|----------|----------|---------|----------|--------|--------|--------|--------|-----|
| Db | 146 | | NTGGYTCSC | TDGYWLL | LEGQCLDI | DECRYGYC | QQLCANV | PGSYSCTC | NP | PGFTLN | EDGRSC | 205 | |
| Qy | 181 | | QDVNECAT | ENPCVQ | TCVNTY | GSFI | CRCDP | GYELED | GVHCSD | MDECSF | SEFLCQ | HECVNQ | 240 |
| Db | 206 | | QDVNECAT | ENPCVQ | TCVNTY | GSFI | CRCDP | GYELED | GVHCSD | MDECSF | SEFLCQ | HECVNQ | 265 |
| Qy | 241 | | PGTYFCSC | PPGYIL | DDNRSC | QDINECE | HRNHTC | NLQQT | CYNLQ | GGFKC | IDPIR | CEEPYL | 300 |
| Db | 266 | | PGTYFCSC | PPGYIL | DDNRSC | QDINECE | HRNHTC | NLQQT | CYNLQ | GGFKC | IDPIR | CEEPYL | 325 |
| Qy | 301 | | RISDNRC | MCPAEN | PGCRDQ | PFTILY | RDMDV | VSGRSV | PADIFQ | MQATTR | YPGAYY | IFQIKS | 360 |
| Db | 326 | | RISDNRC | MCPAEN | PGCRDQ | PFTILY | RDMDV | VSGRSV | PADIFQ | MQATTR | YPGAYY | IFQIKS | 385 |
| Qy | 361 | | GNEGREFY | MRQTGP | ISATLV | MTRPIK | GPRIQL | DLEMIT | TVNTV | INFRG | SSVIRL | RIYVSQ | 420 |
| Db | 386 | | GNEGREFY | MRQTGP | ISATLV | MTRPIK | GPRIQL | DLEMIT | TVNTV | INFRG | SSVIRL | RIYVSQ | 445 |
| Qy | 421 | | YPF | 423 | | | | | | | | | |
| Db | 446 | | YPF | 448 | | | | | | | | | |

RESULT 6

US-10-187-749-408

; Sequence 408, Application US/10187749

; Publication No. US20030153036A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C1

; CURRENT APPLICATION NUMBER: US/10/187,749

; CURRENT FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: US/10/052,586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

```

; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-187-749-408

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Query Match          99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 85

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPTQICI 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPTQICI 145

Qy     121 NTEGGYTCSTDG YWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     146 NTEGGYTCSTDG YWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQUATTRYPGAYYIFQIKS 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQUATTRYPGAYYIFQIKS 385

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
      |||
Db     446 YPF 448

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```

RESULT 7
US-10-194-457-408
; Sequence 408, Application US/10194457
; Publication No. US20030153037A1

```

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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-457-408

```

```

Query Match          99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

QY      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 145

```

Qy 121 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
 |||
 Db 146 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205
 Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
 |||
 Db 206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265
 Qy 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 300
 |||
 Db 266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 325
 Qy 301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
 |||
 Db 326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385
 Qy 361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
 |||
 Db 386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445
 Qy 421 YPF 423
 |||
 Db 446 YPF 448

RESULT 8

US-10-184-642-408

; Sequence 408, Application US/10184642

; Publication No. US20030157635A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C194

; CURRENT APPLICATION NUMBER: US/10/184,642

; CURRENT FILING DATE: 2002-06-27

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-642-408

Query Match 99.8%; Score 2401; DB 12; Length 448;
 Best Local Similarity 99.8%; Pred. No. 9.9e-183;
 Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDI DECRTI PEACRGDMMCVNQNGGYLCI PRTPNPVYRGPYSNPYS | 60 |
| | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDI DECRTI PEACRGDMMCVNQNGGYLCI PRTPNPVYRGPYSNPYS | 85 |
| Qy | 61 | TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI | 145 |
| Qy | 121 | NTEGGYTCSC TDGYWLLEGQCLDI DECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 180 |
| | | | |
| Db | 146 | NTEGGYTCSC TDGYWLLEGQCLDI DECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 205 |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 240 |
| | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 300 |
| | | | |
| Db | 266 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 325 |
| Qy | 301 | RISDNRCMCPAENPGCRDQPF TILYRDMDVVSGRSVPADIFQM QATTRYPGAYYIFQIKS | 360 |
| | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPF TILYRDMDVVSGRSVPADIFQM QATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPIKGP REIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 |
| | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPIKGP REIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 |
| Qy | 421 | YPF 423 | |
| | | | |
| Db | 446 | YPF 448 | |

RESULT 9

US-10-196-747-408

; Sequence 408, Application US/10196747

; Publication No. US20030162250A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C346

; CURRENT APPLICATION NUMBER: US/10/196,747

; CURRENT FILING DATE: 2002-07-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-747-408

Query Match 99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
          |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy     61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 120
          |||
Db     86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 145

Qy    121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
          |||
Db    146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy    181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
          |||
Db    206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy    241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
          |||
Db    266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy    301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
          |||
Db    326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy    361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
          |||
Db    386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy    421 YPF 423
          |||
Db    446 YPF 448
```

RESULT 10

US-10-173-689-408

; Sequence 408, Application US/10173689
; Publication No. US20030166104A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C10
; CURRENT APPLICATION NUMBER: US/10/173,689
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-689-408

Query Match 99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 60
          |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 85

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPQTQICI 120
          |||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPQTQICI 145

Qy     121 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
          |||
Db     146 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
          |||
Db     206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
          |||
Db     266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
          |||
Db     326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
          |||
Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
          |||
Db     446 YPF 448
```

RESULT 11

US-10-173-690-408

; Sequence 408, Application US/10173690
; Publication No. US20030166105A1
; GENERAL INFORMATION:

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C9
; CURRENT APPLICATION NUMBER: US/10/173,690
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-690-408

```

```

Query Match          99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS 60
      |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS 85

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI 120
      |||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI 145

Qy     121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||
Db     146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||
Db     206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      |||
Db     266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQUATTRYPGAYYIFQIKS 360
      |||
Db     326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQUATTRYPGAYYIFQIKS 385

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||
Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423

```

Db |||
446 YPF 448

RESULT 12
US-10-173-691-408
; Sequence 408, Application US/10173691
; Publication No. US20030166106A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C13
; CURRENT APPLICATION NUMBER: US/10/173,691
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-691-408

Query Match 99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 60 |
| | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 85 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI | 145 |
| Qy | 121 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 180 |
| | | | |
| Db | 146 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC | 205 |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 240 |
| | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 300 |
| | | | |
| Db | 266 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 325 |

| | | | | | |
|----|-----|------------------------------|-----------------------------------|-------------------|-----|
| Qy | 301 | RISDNRCMCPAENPGCRDQPF | TILYRDMDVVSGRSVPADIFQM | QATTRYPGAYYIFQIKS | 360 |
| | | | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPF | TILYRDMDVVSGRSVPADIFQM | QATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPIKGP | PREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 | |
| | | | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPIKGP | PREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 | |
| Qy | 421 | YPF | 423 | | |
| | | | | | |
| Db | 446 | YPF | 448 | | |

RESULT 13

US-10-173-692-408

```

; Sequence 408, Application US/10173692
; Publication No. US20030166188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C20
; CURRENT APPLICATION NUMBER: US/10/173,692
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-692-408

```

Query Match 99.8%; Score 2401; DB 12; Length 448;
 Best Local Similarity 99.8%; Pred. No. 9.9e-183;
 Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 60 |
| | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 85 |
| Qy | 61 | TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPQTQICI | 120 |
| | | | |
| Db | 86 | TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPQTQICI | 145 |
| Qy | 121 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGF | 180 |
| | | | |
| Db | 146 | NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGF | 205 |

| | | | |
|----|-----|--|-----|
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 240 |
| | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ | 265 |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 300 |
| | | | |
| Db | 266 | PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL | 325 |
| Qy | 301 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 360 |
| | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 420 |
| | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | 445 |
| Qy | 421 | YPF | 423 |
| | | | |
| Db | 446 | YPF | 448 |

RESULT 14

US-10-173-694-408

; Sequence 408, Application US/10173694

; Publication No. US20030166107A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C19

; CURRENT APPLICATION NUMBER: US/10/173,694

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-173-694-408

Query Match 99.8%; Score 2401; DB 12; Length 448;

Best Local Similarity 99.8%; Pred. No. 9.9e-183;

Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|---|--|----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVQNQGGYLCIPRTNPVYRGPNPYS | 60 |
| | | | |

Db 26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85
 Qy 61 TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 86 TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI 145
 Qy 121 NTEGGYTCSCCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 146 NTEGGYTCSCCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205
 Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 206 QDVNECATENPCVQTCVNTYGSILICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265
 Qy 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325
 Qy 301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385
 Qy 361 GNEGREFYMRQTGPISATLMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 386 GNEGREFYMRQTGPISATLMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445
 Qy 421 YPF 423
 |||
 Db 446 YPF 448

RESULT 15

US-10-173-698-408

; Sequence 408, Application US/10173698

; Publication No. US20030166108A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C12

; CURRENT APPLICATION NUMBER: US/10/173,698

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien
US-10-173-698-408

Query Match 99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy     61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPQTQICI 120
      |||
Db     86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPQTQICI 145

Qy    121 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||
Db    146 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy    181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||
Db    206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy    241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 300
      |||
Db    266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 325

Qy    301 RISDNRCMCPAENPGCRDQPFTILYRMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      |||
Db    326 RISDNRCMCPAENPGCRDQPFTILYRMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy    361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||
Db    386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy    421 YPF 423
      |||
Db    446 YPF 448
```

Search completed: January 9, 2004, 12:43:59
Job time : 29.1676 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:29:16 ; Search time 16.0264 Seconds
(without alignments)
2538.270 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|--------|------------|--------|----|--------|--------------------|
| | | Match | Length | | | |
| 1 | 1108.5 | 46.1 | 493 | 2 | JC5621 | epidermal growth f |
| 2 | 963.5 | 40.0 | 387 | 2 | I38449 | extracellular prot |
| 3 | 744.5 | 30.9 | 685 | 2 | S78040 | fibulin, splice fo |
| 4 | 735.5 | 30.6 | 683 | 2 | C36346 | fibulin 1 precurs |
| 5 | 729.5 | 30.3 | 1221 | 2 | A49457 | fibulin-2 precurs |
| 6 | 702 | 29.2 | 705 | 2 | S34968 | fibulin, splice fo |
| 7 | 701.5 | 29.1 | 1184 | 2 | A55184 | fibulin-2 precurs |
| 8 | 617.5 | 25.7 | 601 | 2 | B36346 | fibulin 1 precurs |
| 9 | 603 | 25.1 | 689 | 2 | T42760 | fibulin, splice fo |
| 10 | 596 | 24.8 | 712 | 2 | T42990 | fibulin 1, splice |
| 11 | 592.5 | 24.6 | 589 | 2 | T43210 | fibulin-1D precurs |
| 12 | 574 | 23.8 | 798 | 2 | T22793 | hypothetical prote |
| 13 | 539 | 22.4 | 1394 | 2 | A35626 | transforming growt |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 14 | 523.5 | 21.7 | 3002 | 2 | A47221 | fibrillin 1 precur |
| 15 | 522.5 | 21.7 | 2871 | 2 | A55567 | fibrillin I - bovi |
| 16 | 518 | 21.5 | 1712 | 2 | A38261 | masking protein pr |
| 17 | 509.5 | 21.2 | 2871 | 2 | A55624 | fibrillin-1 precur |
| 18 | 509.5 | 21.2 | 2907 | 2 | A57278 | fibrillin-2 precur |
| 19 | 508.5 | 21.1 | 2918 | 2 | A54105 | fibrillin-2 precur |
| 20 | 469.5 | 19.5 | 1820 | 2 | A55494 | latent transformin |
| 21 | 455 | 18.9 | 741 | 2 | T46488 | hypothetical prote |
| 22 | 448.5 | 18.6 | 1620 | 2 | T27283 | hypothetical prote |
| 23 | 438 | 18.2 | 1251 | 2 | A57293 | latent transformin |
| 24 | 436 | 18.1 | 1574 | 2 | T13954 | MEGF6 protein - ra |
| 25 | 392 | 16.3 | 886 | 2 | A57172 | probable hormone r |
| 26 | 384.5 | 16.0 | 3507 | 2 | T34513 | hypothetical prote |
| 27 | 368.5 | 15.3 | 1106 | 2 | T18739 | hypothetical prote |
| 28 | 367 | 15.2 | 2471 | 2 | A49128 | cell-fate determin |
| 29 | 364 | 15.1 | 810 | 2 | T10756 | Nel-homolog protei |
| 30 | 361 | 15.0 | 1081 | 2 | T31329 | receptor tyrosine |
| 31 | 359 | 14.9 | 1203 | 2 | A49175 | Notch B protein - |
| 32 | 356 | 14.8 | 2555 | 2 | A40043 | notch protein homo |
| 33 | 353.5 | 14.7 | 1964 | 2 | T09059 | notch4 - mouse |
| 34 | 351.5 | 14.6 | 2437 | 2 | S42612 | transmembrane prot |
| 35 | 348.5 | 14.5 | 2703 | 1 | A24420 | notch protein - fr |
| 36 | 340.5 | 14.1 | 673 | 2 | A48089 | growth arrest-spec |
| 37 | 340 | 14.1 | 2524 | 2 | A35844 | Xotch protein - Af |
| 38 | 335.5 | 13.9 | 2531 | 2 | S18188 | notch protein homo |
| 39 | 335 | 13.9 | 674 | 2 | I55476 | growth potentiatin |
| 40 | 334 | 13.9 | 511 | 2 | T17298 | hypothetical prote |
| 41 | 334 | 13.9 | 2531 | 2 | T31070 | notch homolog - se |
| 42 | 333 | 13.8 | 1064 | 2 | A40136 | fibropellin Ia - s |
| 43 | 333 | 13.8 | 2321 | 2 | S78549 | notch3 protein - h |
| 44 | 325.5 | 13.5 | 2531 | 2 | A46019 | notch-1 protein - |
| 45 | 324.5 | 13.5 | 2318 | 2 | S45306 | notch 3 protein - |

ALIGNMENTS

RESULT 1

JC5621

epidermal growth factor-like protein, T16 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999

C;Accession: JC5621

R;Ozaki, T.; Kondo, K.; Nakamura, Y.; Ichimiya, S.; Nakagawara, A.; Sakiyama, S.
Biochem. Biophys. Res. Commun. 237, 245-250, 1997

A;Title: Interaction of DA41, a DAN-binding protein, with the epidermal growth factor-like protein, S(1-5).

A;Reference number: JC5621; MUID:97415782; PMID:9268694

A;Accession: JC5621

A;Molecule type: mRNA

A;Residues: 1-493 <OZA>

A;Cross-references: DDBJ:D89730; NID:g2429082; PIDN:BAA22265.1; PID:d1023127; PID:g2429083

C;Comment: This protein plays a role in the regulation of cell growth by interacting with DAN protein through DA41 protein.

C;Keywords: glycoprotein

F;1-17/Domain: signal sequence #status predicted <SIG>

F;28-70,158-199,200-237,238-277,278-318,319-359/Region: epidermal growth factor-like repeat

F;249/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.1%; Score 1108.5; DB 2; Length 493;
Best Local Similarity 43.6%; Pred. No. 6.7e-66;
Matches 204; Conservative 68; Mismatches 149; Indels 47; Gaps 5;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPPYSNPYS 60
      |||:|::| || ||||| :|:|:| ||| |||||:|:| :
Db      28 QCTDGYEWDVPVRQQCKDIDECDIVPDACKGGMKCVNHYGGYLCPLKTAQIIVNNEQPQQE 87

Qy      61 TPYS-----GYPYAAAPPLSAPNYPT----- 81
      || : ||:|:| :|:| |
Db      88 TPAAEASSGAATGTIAARSMATSGVIPGGGFIAATAVAGPEVQTGRNNFVIRRNADPQ 147

Qy      82 -----ISRPLICRFGYQMDESNCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWL 136
      | : | ||:| ||| :|:| :|:| | :||| | :||| ||
Db      148 RIPSNPISHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRLDQVCINLRGSFTCHCLPGYQK 207

Qy      137 LEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQT 195
      ||:||||| || ||| |||:| ||||| | : :| |:||| |||
Db      208 RGEQCVDIDECVPPYCHQGCVNTPGSFYQCNPGFQLAANNYTCVDINECDASNQCAQQ 267

Qy      196 CVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILL 255
      | | |||||:|:| |||| | :|:| |:||| | :|||:|:|:|:| :| ||| || :
Db      268 CYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCPQGYQVV 327

Qy      256 DDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPG 315
      :|:||||||| | | :|:| |||:| | :||:| |:|||:| |
Db      328 -RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPQNPCQDPYVLTSENRCVCPVSNTM 385

Qy      316 CRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPI 375
      ||| | :|:|:| :|:| | ||||:||||:|||| | | :||||| |||:||| |
Db      386 CRDVPQSIVYKYMNI RSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYLRQTSPV 445

Qy      376 SATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      || ||: : : |||| : |||:|:|:| || |||:| | | : |
Db      446 SAMLVLVKSLTGPREHIVGLEMLTVSSIGTFR TSSVLRLTIIVGPFSF 493
```

RESULT 2

I38449

extracellular protein - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C;Accession: I38449

R;Lecka-Czernik, B.; Lumpkin, C.K.

Mol. Cell. Biol. 15, 120-128, 1995

A;Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts encoding a novel protein in the epidermal growth factor-like repeat family stimulates DNA synthesis.

A;Reference number: I38449; MUID:95097983; PMID:7799918

A;Accession: I38449

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-387 <RES>

A;Cross-references: EMBL:U03877; NID:g458227; PIDN:AAA65590.1; PID:g458228
C;Genetics:
A;Gene: S1-5

Query Match 40.0%; Score 963.5; DB 2; Length 387;
Best Local Similarity 48.3%; Pred. No. 1.9e-56;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

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Qy      71 APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICINTEGGYTCS 130
      | | | | | : | | | : | | | : | | | : | | | : | | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 189
      | | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCSPGFQLAANNYTQVDINECDAS 155

Qy     190 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPQGTFCSCP 249
      | | | | | | | | | | | | | | | | | | | | | | |
Db     156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy     250 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEYPYLRISDNRCMC 309
      | | : : : | | | | | | | | | | | | | | | | | |
Db     216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPEINRCVC 273

Qy     310 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 369
      | | | | | : | : | : | : | | | | | | | | | | |
Db     274 PVSNAMELPQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGFEFYL 333

Qy     370 RQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | : | | | | : : : | | | | : | | | | : | |
Db     334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 387
```

RESULT 3

S78040

fibulin, splice form C precursor - mouse

N;Alternate names: basement-membrane protein BM-90

C;Species: Mus musculus (house mouse)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 02-Aug-2002

C;Accession: S78040; S78560; S36440

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

Eur. J. Biochem. 215, 733-740, 1993

A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement-membrane ligands.

A;Reference number: S34968; MUID:93358897; PMID:8354280

A;Accession: S78040

A;Molecule type: mRNA

A;Residues: 1-685 <PAN>

A;Cross-references: EMBL:X70854

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

submitted to the EMBL Data Library, January 1993

A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement membrane ligands.

A;Reference number: S36440

A;Accession: S78560

A;Molecule type: mRNA

A;Residues: 1-39,'P',41-685 <CHU>

A;Cross-references: EMBL:X70854
 C;Genetics:
 A;Introns: 568/3
 C;Superfamily: fibulin-1; EGF homology
 C;Keywords: alternative splicing; basement membrane; calcium binding;
 extracellular matrix; glycoprotein; plasma
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-685/Product: fibulin, splice form C #status predicted <MAT>
 F;98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.9%; Score 744.5; DB 2; Length 685;
 Best Local Similarity 36.6%; Pred. No. 8.3e-42;
 Matches 159; Conservative 63; Mismatches 151; Indels 61; Gaps 16;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS 60
      || :|| | | | :|||:| | | | | | | | | |
Db      295 QCKSGFIQD-ALGNCIDINECLSISAPCPVGQTCINTEGSYTC----- 336

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | | : | | : ||||| | | : | |
Db      337 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHHC 375

Qy      120 INTEGgyTCsCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYsCTCNPGFTLN 174
      :| : | | | : : | :||:| | | | | | | | | | :| :| :| | | :
Db      376 LNSPGSFRCECKAGFYFDGISRTCVDINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS 435

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SEF 231
      |||||:|||| | :|| | | | |||: | | ||: | : || | | :||| :
Db      436 VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 494

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCI 290
      : | : | :| |||: || | | : |||||: | | | : : ||:| :| | | :| :
Db      495 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL 554

Qy      291 DPIRCEEPYLRISDNRCM--CPAENPGCRDQPFITILYRMDVVSGRSVPADIFQMATT 347
      | | | | :| | | | | | | | | | : | : | | :| :| :| :
Db      555 S-FECPENYRRSADTRCARLPC-HENQECPRLPRLITYYHLSFPTNIQVPAVFRMGPS 612

Qy      348 RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEM--ITVNTVIN 405
      || | | :|| | | | : | : :|:| | ||: | :| | | | :
Db      613 AVPGDSMQLAITAGNEEGFFTTRKVS HSGVVALTKPIPEPRDLLLTVKMDLYRHGTVSS 672

Qy      406 FRGSSVIRLRIYVS 419
      | | | :| | |
Db      673 F----VAKLFIFVS 682

```

RESULT 4
 C36346
 fibulin 1 precursor, splice form C - human
 N;Alternate names: fibulin C
 N;Contains: fibulin 1 splice form A; fibulin 1 splice form C
 C;Species: Homo sapiens (man)
 C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 02-Aug-2002
 C;Accession: C36346; A36346; A32826
 R;Argaves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
 J. Cell Biol. 111, 3155-3164, 1990

A;Title: Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure.
A;Reference number: A36346; MUID:91100426; PMID:2269669
A;Accession: C36346
A;Molecule type: mRNA
A;Residues: 1-683 <ARG>
A;Cross-references: GB:X53743; NID:g31418; PIDN:CAA37772.1; PID:g31419
A;Accession: A36346
A;Molecule type: mRNA
A;Residues: 1-566 <AR2>
A;Cross-references: GB:X53741; NID:g31414; PIDN:CAA37770.1; PID:g31415
R;Argaves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E.
Cell 58, 623-629, 1989
A;Title: Fibulin, a novel protein that interacts with the fibronectin receptor beta-subunit cytoplasmic domain.
A;Reference number: A32826; MUID:89354537; PMID:2527614
A;Accession: A32826
A;Molecule type: protein
A;Residues: 30-35, 'SX', 38-40, 'SH', 43-44 <AR3>
C;Genetics:
A;Gene: GDB:FBLN1; FBLN
A;Cross-references: GDB:278285; OMIM:135820
A;Map position: 22q13.3-22q13.3
C;Superfamily: fibulin-1; EGF homology
C;Keywords: alternative splicing; glycoprotein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-683/Product: fibulin 1 splice form C #status predicted <MAT>
F;180-214/Domain: EGF homology <EGF>
F;485-523/Domain: EGF homology <EGF1>
F;98,535,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.6%; Score 735.5; DB 2; Length 683;
Best Local Similarity 35.7%; Pred. No. 3.2e-41;
Matches 155; Conservative 66; Mismatches 152; Indels 61; Gaps 16;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      || :|| | | :|:|:| | :| | | | |
Db      293 QCKSGFIQD-ALGNCIDINECLISAPCPIGHTCINTEGSYTC----- 334

Qy      61 TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | : | : ||||| | : | |
Db      335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 373

Qy      120 INTEGgyTCSCTDGYWL--LEGQCLDIDEc-RY--GYCQQLCANVPGSYsCTCNPGFTLN 174
      :|: | : | | ||: : | :|:| | | | | | | | | | | | | |
Db      374 VNspGSFRCECKTGYyFDGISRMcVDVNEcQRYpGRlCGHKCENTlGSyLCSsVGfRLS 433

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SEF 231
      |||||:|:|:|:|:| | | | | | | | | | | | | | | |
Db      434 VDGRsCEDINEcSS-SPcSQECANvYGSyQYcCRRGYQLSDVDGVTcEDIDECALPTGGH 492

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTcYNLQGGFKCI 290
      :| : | : | | | | | | : | : | | | | | | | | | | | |
Db      493 ICSYRCINIPGSFQcSCPSSGYRLAPNGRNCQDIDEcVTGIHNcSINETcFNlQGAfRCL 552

Qy      291 DPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPADIFQMqATTR 348
      | | | | : | | | | | | | | : : | | : | : |

```

```

Db      553 -AFECPENYRRSAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPAVVFRMGPSA 611
Qy      349 YPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRG 408
        ||      |  |||  |  |:  |  |  :  :|:|:  ||::  ::||  ::  |
Db      612 VPGDSMQLAITGGNEEGFFTTRKVSPhSGVVALTKPVPEPRDL-----LLTVKMDLSRHG 666

Qy      409 ---SSVIRLRIYVS 419
        |  |  :|  |:|
Db      667 TVSSFVAKLFIFVS 680

```

RESULT 5

A49457

fibulin-2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Sep-2002

C;Accession: A49457; S74095

R;Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.
J. Cell Biol. 123, 1269-1277, 1993

A;Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with multiple EGF-like repeats and consensus motifs for calcium binding.

A;Reference number: A49457; MUID:94064787; PMID:8245130

A;Accession: A49457

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1221 <PAN>

A;Cross-references: GB:X75285; NID:g437046; PIDN:CAA53040.1; PID:g437047

R;Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.

Eur. J. Biochem. 240, 427-434, 1996

A;Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix metalloproteinases and other tissue proteases.

A;Reference number: S74094; MUID:96439073; PMID:8841408

A;Accession: S74095

A;Molecule type: protein

A;Residues: 236-238,'X',240-247;260-275;336-344,'L',346-361;405-426;566-568,'EM',569-589;653-666;784-787,'X',789-794;841-844,'X',846-850;883-892,'X',894-894;930-935,'X',937-939 <SAS>

C;Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology

C;Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer

F;942-978/Domain: EGF homology <EGF>

```

Query Match          30.3%;  Score 729.5;  DB 2;  Length 1221;
Best Local Similarity 35.3%;  Pred. No. 1.3e-40;
Matches 145;  Conservative 59;  Mismatches 148;  Indels 59;  Gaps 11;

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```

Qy      1  QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS 60
        :| :|| |  |  |:|:|:|:|  ::  |  ||  |:|  |  |  |
Db      832 RCMDGF-LQDPEGNCVDINECTSLLEPCRSGFSCINTVGSYTC----- 873

Qy      61  TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC 119
        ||:|  ||  :|  ::|||:|  |  |:|  |:|
Db      874 -----QRNPLVCGRGYHANEEGSECVDVNECETGVHRCGEGQLC 912

Qy      120 INTEGTYTCSDTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGFTLN 174
        |  |  |  |  |  |  :  |  :|:|:|  |  |  |  |  |  |  |  |

```

| | | | |
|----|------|---|------|
| Db | 913 | YNLPGSYRCDCKPGFQRDAFGRTCIDVNECWVSPGRLCQHTCENTPGSYRCSAAGFLLA | 972 |
| Qy | 175 | EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC | 233 |
| Db | 973 | ADGKHCEDVNECETR-SCQECAIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC | 1031 |
| Qy | 234 | QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDP | 292 |
| Db | 1032 | TFRCVNVPGSYQCACPEQGYTMMANGRSCKDLDECALGTHNCSEAETCHNIQGSFRCL-R | 1090 |
| Qy | 293 | IRCEEPYLRI SDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQM QAT | 346 |
| Db | 1091 | FDCPPNYVRVSQTKC----ERTTCQDITECQTSPARITHYQLNFQTGLLVPAHIFRIGPA | 1146 |
| Qy | 347 | TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM | 397 |
| Db | 1147 | PAFAGDTISLTI TKGNEEGYFVTRRLNAYTGVSLSLQSVLEPRDFALDVEM | 1197 |

F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-705/Product: fibulin, splice form D #status predicted <MAT>
 F;98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.2%; Score 702; DB 2; Length 705;
 Best Local Similarity 35.2%; Pred. No. 5.4e-39;
 Matches 160; Conservative 66; Mismatches 154; Indels 74; Gaps 21;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 60
      || :|| | | | :||| :| | | | :| | |
Db      295 QCKSGFIQD-ALGNCIDINECLSIAPCPVGQTCINTEGSYTC----- 336

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | | :| :||| | | :| | | | | :| |
Db      337 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHC 375

Qy      120 INTEGgyTCsCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYsCTCNPGFTLN 174
      :| : | | | :| : | | | | | | | | | | :| :| :| | |
Db      376 LNSPGSFRCECKAGFYFDGISRTCDVINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS 435

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SEF 231
      ||||| :||| | | | | | :| | | | :| | | | :| | |
Db      436 VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 494

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI 290
      :| : | :| ||| :| | | | :| :||| :| | | | | :| :| :| :|
Db      495 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL 554

Qy      291 DPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFTILYRDMDVVSGRSV-- 336
      | | | | :| | | | :| | :| | | :| :| :| :|
Db      555 S-FECPENYRRSADTFRQEKTDTVRCIKSCRPNDEACVRDPVHTVSHTVISLPTFREFTR 613

Qy      337 PADIFQMQATT-RYPG--AYYIFQIKSGNEGREFYM---RQTGPISATLVMTRPIKGP 390
      | :| :| :| | | | | | | | | | :| :| :| :|
Db      614 PEEIIFLRAVTPLYPANQADIIFDITEGNLRDSFDIIKRYEDGMTVGVRQVRPIVGP 673

Qy      391 IQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | :| :| :| :| :| :| :|
Db      674 AVLKLEMNYVLGGVVSHR--NVNVNHIFVSEYWF 705

```

RESULT 7

A55184

fibulin-2 precursor - human

N;Alternate names: protein DKFZp586A1519.1

C;Species: Homo sapiens (man)

C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 08-Sep-2002

C;Accession: A55184; T08744

R;Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Chu, M.L.

Genomics 22, 425-430, 1994

A;Title: Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping of the gene on human and mouse chromosomes.

A;Reference number: A55184; MUID:95104855; PMID:7806230

A;Accession: A55184

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1184 <ZHA>

A;Cross-references: GB:X82494; NID:g575232; PIDN:CAA57876.1; PID:g575233
 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, March 1999
 A;Reference number: Z16471
 A;Accession: T08744
 A;Molecule type: mRNA
 A;Residues: 656-719, 'QDECLMGAHDCSRRQFCVNTLGSFYCVNHTVLCADGYILNAHRKCVD', 720-
 853, 'T', 855-1184 <WAM>
 A;Cross-references: EMBL:AL050095
 A;Experimental source: adult uterus; clone DKFZp586A1519
 C;Genetics:
 A;Gene: GDB:FBLN2
 A;Cross-references: GDB:293037; OMIM:135821
 A;Map position: 3p25-3p24
 A;Note: DKFZp586A1519.1
 C;Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat
 homology
 C;Keywords: alternative splicing; extracellular matrix
 F;1-27/Domain: signal sequence #status predicted <SIG>
 F;28-1184/Product: fibulin-2 protein #status predicted <MAT>
 F;905-941/Domain: EGF homology <EGF>

Query Match 29.1%; Score 701.5; DB 2; Length 1184;
 Best Local Similarity 34.5%; Pred. No. 9.1e-39;
 Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 60.
      :| :|| | | :|:|:| :| :| | | :| | | |
Db      795 RCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC----- 836

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHQCNPTQIC 119
      ||| | | | :| :|:|:| | | :| | | :|
Db      837 -----QRNPLICARGYHASDDGAKCVDVNECETGVHRCGEGQVC 875

Qy      120 INTEGgyTCsCTDgyw--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGFTLN 174
      | | | | | :| :|:|:| | | | | | | | :| | |
Db      876 HNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENTLGSYRCSASCAGFLLA 935

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC 233
      ||: |:|:| | :| | | | | | :| | | | | :|:|:| :|
Db      936 ADGKRCEdVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC 994

Qy      234 QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDP 292
      |:| |:|:| |:| | | :| :|:|:|:| | | :| :|:|:| | |:|
Db      995 TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R 1053

Qy      293 IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT 346
      | | :|:| :| | | | | | | :| :| :| :| | | | :|
Db      1054 FECPPNYVQVSKTKC----ERTTCHDFLEcQNSPARITHYQLNFQTGLLVPAHIFRIGPA 1109

Qy      347 TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM 397
      :| | | | | | :| :| :| :| :| :| :|
Db      1110 PAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLQRAVLEPRDFALDDEM 1160

```

fibulin 1 precursor, splice form B - human
 C;Species: Homo sapiens (man)
 C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 02-Aug-2002
 C;Accession: B36346
 R;Argaves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
 J. Cell Biol. 111, 3155-3164, 1990
 A;Title: Fibulin is an extracellular matrix and plasma glycoprotein with
 repeated domain structure.
 A;Reference number: A36346; MUID:91100426; PMID:2269669
 A;Accession: B36346
 A;Molecule type: mRNA
 A;Residues: 1-601 <ARG>
 A;Cross-references: GB:X53742; NID:g31416; PIDN:CAA37771.1; PID:g31417
 C;Genetics:
 A;Gene: GDB:FBLN1; FBLN
 A;Cross-references: GDB:278285; OMIM:135820
 A;Map position: 22q13.3-22q13.3
 C;Superfamily: fibulin-1; EGF homology
 C;Keywords: alternative splicing
 F;180-214/Domain: EGF homology <EGF1>
 F;485-523/Domain: EGF homology <EGF>

Query Match 25.7%; Score 617.5; DB 2; Length 601;
 Best Local Similarity 38.3%; Pred. No. 1.7e-33;
 Matches 119; Conservative 46; Mismatches 95; Indels 51; Gaps 12;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      || :|| | | :|:|:| | :| | | | |
Db      293 QCKSGFIQD-ALGNCIDINECLISAPCPIGHTCINTEGSYTC----- 334

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | | :| :|:| | | | : | |
Db      335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 373

Qy      120 INTEGgyTCSTdgyWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
      :| : | | || : | :|:| | | | | | | | | | | |
Db      374 VNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS 433

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDMECSF--SEF 231
      |||||:|:|:|:|:| | | | | | | | | | | | | |
Db      434 VDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 492

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI 290
      :| : | :| ||:| || | : | :|:| | | | | | | | |
Db      493 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGAFRCL 552

Qy      291 DPIRCEEPYLR 301
      | | | |
Db      553 -AFECPENYRR 562

```

RESULT 9

T42760

fibulin, splice form D precursor - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 23-Sep-2002

C;Accession: T42760

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
submitted to the EMBL Data Library, February 1998

A;Description: Isolation of chicken and nematode fibulin-1 homologs and
characterization of the nematode fibulin-1 gene.

A;Reference number: Z22267

A;Accession: T42760

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-689 <BAR>

A;Cross-references: EMBL:AF051401; PIDN:AAC28321.1

C;Genetics:

A;Note: FBLN1

Query Match 25.1%; Score 603; DB 2; Length 689;
Best Local Similarity 27.4%; Pred. No. 1.7e-32;
Matches 156; Conservative 52; Mismatches 155; Indels 206; Gaps 19;

```
Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCNVNQGGYLCIPRTNPVYRGPYSNPYST 61
      | : ||| | | : ||| | | : : | : | | : | |
Db     180 CRSGFDLAPDGMACVDIDECATLMDDCLESQRCLNTPGSFKCI----- 222

Qy      62 PYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHQCNPTQICI 120
      | | | | | | | : : | | | | | | | | |
Db     223 -----RTLSCGTGYAMDSETERCRDVDECNLGSHDCGPLYQCR 260

Qy     121 NTEGGYTC-----SCTDGYWLLEGQCLDIDECRYGY----- 151
      ||:| | | : | : ||: | | | | | | :
Db     261 NTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDIDECVTGHNCGAGEEC 320

Qy     152 -----CQQ---LCA-----NVPGSYSCTCNPGF 171
      ||| | | | | | | | | | | | | | |
Db     321 VNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPGTYKCKCGPGY 380

Qy     172 TLNE-----DGRSCQDVNECA 187
      | : | | | | | | | | | | |
Db     381 EFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNECT 440

Qy     188 TE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF----SEFLCQHECVNQPG 242
      | | | | | | | : | | | : | | | | | | | | | | |
Db     441 TGIAACEQKCVNIPGSYQICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTKG 500

Qy     243 TYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRI 302
      : | | | | | : | | : | : | | : | | | | | | |
Db     501 SYLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYIHD 558

Qy     303 SDNR-----C--MCPAENPGC-RDQPFTILYRDMDVVSGRSV--PADI----- 340
      | | : | : | : | : : | | : : | :
Db     559 SLNKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTIIISPIEVSRIVTHMGV 618

Qy     341 -FQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMIT 399
      | : | | : : | | : : | | | : | |
Db     619 PFSVDYNLDYVGQRHFRIVQERNIG-----IVQLVKPISGP-----TVETIK 660

Qy     400 VNTVINFRGSSVIR-----LRIYVSQYPF 423
      || | | : : | | | | |
Db     661 VNIHTKSRTGVILAFNEAIIIEISVSKYPF 689
```

RESULT 10

T42990

fibulin 1, splice form C precursor - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 08-Sep-2002

C;Accession: T42990

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
submitted to the EMBL Data Library, February 1998

A;Description: Isolation of chicken and nematode fibulin-1 homologs and
characterization of the nematode fibulin-1 gene.

A;Reference number: Z22267

A;Accession: T42990

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-712 <BAR>

A;Cross-references: EMBL:AF051402; PIDN:AAC28322.1

C;Genetics:

A;Gene: FBLN1

C;Superfamily: fibulin-1; EGF homology

C;Keywords: alternative splicing; basement membrane; extracellular matrix

Query Match 24.8%; Score 596; DB 2; Length 712;
Best Local Similarity 27.9%; Pred. No. 5.1e-32;
Matches 152; Conservative 46; Mismatches 145; Indels 202; Gaps 18;

```

Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCQNQGGYLCIPRTNPVYRGPYSNPYST 61
      | : ||| | | : ||| | | : : | | : | | : ||
Db     180 CRSGFDLAPDGMACVDIDECATLMDDCLESQRCLNTPGSFKCI----- 222

Qy      62 PYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHQCNPQTQICI 120
      | | | | | | | | | | : | | | | | | | | | |
Db     223 -----RTLSCGTGYAMDSETERCRDVDECNLGSHDCGPLYQCR 260

Qy     121 NTEGGYTC-----SCTDGYWLLEGQCLDIDECRYGY----- 151
      ||:| | | | : | : ||: | | | | | | | :
Db     261 NTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDIDECVTGHNCGAGEEC 320

Qy     152 -----CQQ---LCA-----NVPGSYSCTCNPGF 171
      ||| | | | | | | | | | | | | | | | | |
Db     321 VNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPGTYKCKCGPGY 380

Qy     172 TLNE-----DGRSCQDVNECA 187
      | : | | | | | | | | | | | | | |
Db     381 EFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNECT 440

Qy     188 TE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF----SEFLCQHECVNQPG 242
      | | | | | | | | | | : | | | | | | | | | |
Db     441 TGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTKG 500

Qy     243 TYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRI 302
      : | | | | | | : | | | | : | | | | | | | :
Db     501 SYLCQCPPGYKIQPDGRTCDVDDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYIHD 558

Qy     303 SDNR-----CMCPAENPGCRDQPFITILYRDMDVVSGRSVP----- 337
      | | : | | | | | | | | : | : : : | : |
Db     559 SLNKNRCNRQPSACGLPEE---CSKVPLFLTYQFISL--ARAVPISSHRPAITLFKVSAP 613

```

Qy 338 --ADI---FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISATLVMTRPIKGP 390
 || |::| | || : |::| | | : : : ||:
 Db 614 NHADTEVNFELQLKTTIVGAPNVLP AIRAN-----FLLQKGEKRNSAVVTLRDSL DGPQT 668
 Qy 391 IQLDL 395
 : : | |
 Db 669 VKLQL 673

RESULT 11

T43210

fibulin-1D precursor - *Caenorhabditis elegans* (fragment)

C;Species: *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 08-Sep-2002

C;Accession: T43210

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
 submitted to the EMBL Data Library, June 1998

A;Description: Identification of chicken and *C. elegans* fibulin-1 homologs and
 characterization of the *C. elegans* fibulin-1 gene.

A;Reference number: Z22337

A;Accession: T43210

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-589 <BAR>

A;Cross-references: EMBL:AF070477; PIDN:AAC24035.1

C;Genetics:

A;Note: intron positions not resolved (incomplete sequence)

C;Superfamily: fibulin-1; EGF homology

Query Match 24.6%; Score 592.5; DB 2; Length 589;
 Best Local Similarity 27.4%; Pred. No. 7.4e-32;
 Matches 156; Conservative 52; Mismatches 155; Indels 207; Gaps 20;

Qy 2 CTNGFDLDRQSGQCLD-IDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
 | : ||| | : | ||| | : : | : | : | |
 Db 79 CRSGFDLAPDGMACVDHIDECATLMDDCLESQRCLNTPGSFKCI----- 122
 Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHCNPTQIC 119
 | | | | | | : : | ||| | | | | | |
 Db 123 -----RTLSCGTGYAMDSETERCDVDECNLGSHDCGPLYQC 159
 Qy 120 INTEGgyTC-----SCTDGYWLLEGQCLDIDECRYGY----- 151
 || : | | : | : || : | | ||| | :
 Db 160 RNTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDIDECVTGHNCGAGEE 219
 Qy 152 -----CQQ---LCA-----NVPGSYSCTCNPG 170
 || | || | : || : | | | |
 Db 220 CVNTPGSFRCCQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPGTYKCKCGPG 279
 Qy 171 FTLNE-----DGRSCQDVNEC 186
 : : || | : ||| |
 Db 280 YEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNEC 339
 Qy 187 ATE-NPCVQTCVNtyGSFICRCDPGYELEDGVHCSMDDECSF-----SEFLCQHECVNQP 241
 | | | | | : | | : | | | : ||| | | : |
 Db 340 TTGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTK 399

```

Qy      242 GTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLR 301
          | : | | | | | : | | : | | : | | : | | | | | | : |
Db      400 GSYLCQCPPGYKIQPDGRTCDVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYIH 457

Qy      302 ISDNR-----C--MCPAENPGC-RDQPFTILYRDMDVVSGRSV--PADI----- 340
          | | : | : | | : | : | | : | | : | : |
Db      458 DSLNKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTII SPIEVSRIVTHMG 517

Qy      341 --FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMI 398
          | : | | : : | | : : : | | | : | |
Db      518 VPFSVDYNLDYVGQRHFRIVQERNIG-----IVQLVKPISGP-----TVETI 559

Qy      399 TVNTVINFRGSSVIR-----LRIYVSQYPF 423
          | | | | : : : | | | | |
Db      560 KVNHTKSRTGVILAFNEAII EISVSKYPF 589

```

RESULT 12

T22793

hypothetical protein F56H11.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002

C;Accession: T22793; T24489

R;Wilkinson, J.

submitted to the EMBL Data Library, January 1996

A;Reference number: Z19616

A;Accession: T22793

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-798 <WIL>

A;Cross-references: EMBL:Z68749; PIDN:CAA92962.1; GSPDB:GN00022; CESP:F56H11.1

A;Experimental source: clone F56H11

R;Lloyd, C.

submitted to the EMBL Data Library, December 1995

A;Reference number: Z19897

A;Accession: T24489

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-798 <WI2>

A;Cross-references: EMBL:Z68219; PIDN:CAA92483.1; GSPDB:GN00022; CESP:F56H11.1

A;Experimental source: clone T05A1

C;Genetics:

A;Gene: CESP:F56H11.1

A;Map position: 4

A;Introns: 14/1; 92/3; 144/1; 195/1; 281/1; 325/2; 371/2; 390/1; 437/1; 471/3;
498/3; 607/1; 649/2; 718/1

C;Superfamily: fibulin-1; EGF homology

Query Match 23.8%; Score 574; DB 2; Length 798;

Best Local Similarity 26.8%; Pred. No. 1.6e-30;

Matches 159; Conservative 49; Mismatches 172; Indels 214; Gaps 22;

```

Qy      2 CTNGFDLDRQSGQCLDI DECRTIPEACRGDMMCVNQNGGYLC-----IP---RTNPVY 51
          | : | | | | | : | | : | | | | | | | | : | | :
Db      180 CRSGFDLAPDGMACVDRNECLTRQSPCTQSEDCVNTIGGYICQRRISRLVPHRHRANRIG 239

```

RESULT 13

transforming growth factor beta-1-binding protein - human

C;Date: 21-Sep-1990 #sequence revision 21-Sep-1990 #text change 11-Jan-2000

R;Kanzaki, T.; Olofsson, A.; Moren, A.; Wernstedt, C.; Hellman, U.; Miyazono, K.; Claesson-Welsh, L.; Heldin, C.H.

A;Title: TGF-beta1 binding protein: a component of the large latent complex of TGF-beta1 with multiple repeat sequences.

A;Status: preliminary; not compared with conceptual translation

A;Cross-references: GB:M34057; NID:q339547; PIDN:AAA61160.1; PID:q339548

C;Keywords: alternative splicing

F;750-791/Domain: EGF homology <EGF>

Query Match 22.4%; Score 539; DB 2; Length 1394;
 Best Local Similarity 29.6%; Pred. No. 5.3e-28;
 Matches 126; Conservative 51; Mismatches 126; Indels 122; Gaps 17;

```

Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCIPRTNPVYRGPYSNPYST 61
      |  | :  |  | :|:|||| |  |  |  |  | :|||
Db      573 CYEGYRFSEQQRKCVDIDECTQVQHLC-SQGRCENTEGSF LCI----- 614

Qy      62 PYSGPYPAAPPLSAPNYPTISRPLI-----CRFGYQMDENQCVDVD 104
      :  | :  :  :  |  |  |  |  |  |  |  | :  | :  | :  |
Db      615 -CPAGFMASEEGTNCIDVDECLRPDVCGEHCVNTVGAFRCEYCDSGYRMTQGRCEDID 673

Qy      105 ECATDSHQCNPTQICINTEGGYTC-SCTDGYWLLEGQCLDIDEC-RYGYCQQ-LCANVPG 161
      ||  |  |  |  | :|:| |  |  |  |  | :|:| |  |  |  |  |  |  | :|:| |
Db      674 ECLNPS-TC-PDEQCVNSPGSYQCVPCTEGFRGWNGQCLDVDECLPNVCANGDCSNLEG 731

Qy      162 SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQ----- 194
      || | :| :| |  | : | :| :| |  |  |  |
Db      732 SYMCSCHKGYTRTPDHKHCRDIDECQQGNLCVNGQCKNTEGSFRCTCGQGYQLSAAKDQC 791

Qy      195 -----TCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQH-ECV 238
      |  |  |  |  |  |  |  |  |  |  |  |  |  | :|:| |  :  | :| :| :|
Db      792 EDIDECQHRHLCAHGQCRNTEGSFQCVCDDQGYRASGLGDHCEIDINECLEDKSVCQRGDCI 851

Qy      239 NQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI----- 290
      |  | :| | :| | | : | | | :| | | | | |  |  |  |  | :| | | :|
Db      852 NTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEGSFHCVCQQGFSIS 909

Qy      291 -DPIRCEEPYLRI-----DN-----RCMC-----PAENPGCRDQPFTILYRDM 328
      |  |  | :  :  |  |  |  |  |  |  |  | :  |  |  |  |  |
Db      910 ADGRTCEDIDECVNNTVCDSHGFCDNTAGSFRCLCYQGFQAPQDQGQCVD-----VNEC 963

Qy      329 DVVSG 333
      : : : | |
Db      964 ELLSG 968
  
```

RESULT 14

A47221

fibrillin 1 precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002

C;Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

Genomics 17, 476-484, 1993

A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure and alternatively spliced exons at the 5' end.

A;Reference number: A47221; MUID:94010947; PMID:7691719

A;Accession: A47221

A;Molecule type: mRNA

A;Residues: 1-337,'T',339-1029 <COR>

A;Cross-references: GB:X63556

R;Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangilinan, T.; Bonadio, J.

Hum. Mol. Genet. 2, 961-968, 1993

A;Title: Genomic organization of the sequence coding for fibrillin, the defective gene product in Marfan syndrome.
 A;Reference number: I54355; MUID:93372860; PMID:8364578
 A;Accession: I54355
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 132-3002 <PER>
 A;Cross-references: GB:L13923; NID:g306745; PIDN:AAB02036.1; PID:g306746
 R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y. Nature 352, 334-337, 1991
 A;Title: Partial sequence of a candidate gene for the Marfan syndrome.
 A;Reference number: S17064; MUID:91304568; PMID:1852207
 A;Accession: S17064
 A;Molecule type: mRNA
 A;Residues: 1030-3002 <MAS>
 A;Cross-references: EMBL:X63556
 R;Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J. Science 259, 680-683, 1993
 A;Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
 A;Reference number: I59574; MUID:93157831; PMID:8430317
 A;Accession: I59574
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 2217-2288, 'I', 2290-2325 <RES>
 A;Cross-references: GB:S54426; NID:g264860; PIDN:AAB25244.1; PID:g264861
 R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.; Ramirez, F.; Hollister, D.W. Nature 352, 330-334, 1991
 A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different fibrillin genes.
 A;Reference number: S17062; MUID:91304567; PMID:1852206
 A;Accession: S17062
 A;Molecule type: mRNA
 A;Residues: 'VLVTVFIFLSYNKML', 944-1444 <LEE1>
 A;Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB56534.1; PID:g5924015
 A;Accession: S62111
 A;Molecule type: protein
 A;Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEE2>
 R;Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W. J. Biol. Chem. 264, 21381-21385, 1989
 A;Title: Connective tissue microfibrils. Isolation and characterization of three large pepsin-resistant domains of fibrillin.
 A;Reference number: A34198; MUID:90078246; PMID:2512293
 A;Accession: A34198
 A;Molecule type: protein
 A;Residues: 565-575; 1890-1892, 'I', 1894-1900 <MAD>
 C;Comment: Fibrillin is a major component of elastin-associated microfibrils.
 C;Genetics:
 A;Gene: GDB:FBN1
 A;Cross-references: GDB:127115; OMIM:134797; OMIM:154700
 A;Map position: 15q21.1-15q21.1
 A;Introns: 2236/1; 2258/1; 2297/1
 C;Superfamily: fibrillin 1; EGF homology
 C;Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; Marfan syndrome

F;1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predicted <MATA>
 F;132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC>
 F;1332-1367/Domain: EGF homology <EGF>
 F;1457-1492/Domain: EGF homology <EGF2>
 F;2262-2295/Domain: EGF homology <EGF1>

Query Match 21.7%; Score 523.5; DB 2; Length 3002;
 Best Local Similarity 30.3%; Pred. No. 1.1e-26;
 Matches 122; Conservative 47; Mismatches 120; Indels 113; Gaps 18;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      :| :|| || : | ||||| | : | | || | : | : | :
Db      1185 RCDSGFALDSEERNCTDIDECRISPDLG-GRGQCVNTPGDFEC--KCDEGYESGF----- 1236

Qy      61 TPYSGPYPAAPPLSAPNYPTISR----PLICRF-----GYQMDSE-NQ 99
      : | | | ||:| |
Db      1237 -----MMMKNCMDIDECQRDPLLCRGGVCHNTEGSYRCECPGHLSPNISA 1283

Qy      100 CVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQ--CLDIDECRY--GYCQQL 155
      |:|::|| :| | | |:| | | |:| || : |:| |||| | | :
Db      1284 CIDINECELSAHLG-PNGRCVNLIQKYQCACNPGYHSTPDRLFCVDIDECSIMNGGCETF 1342

Qy      156 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENP----- 191
      | | ||| |:| ||| | | ||| |:| | :|
Db      1343 CTNSEGSYECSCQPGFALMPDQSRCTDIDEC-EDNPNICDGGQCTNIPGEYRCLCYDGM 1401

Qy      192 -----CVQ-----TCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSE 230
      || || || |||| | | || : : |:|::||
Db      1402 ASEDMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA 1461

Qy      231 FLC-QHE-CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFK 288
      | :| | | |:| ||| |:| | | |:| | : | | :|
Db      1462 HNCCKHVACTNTAGSFKCSCSPGWI--GDGIKCTDLDECSNGTHMCSQHADCKNTMGSYR 1519

Qy      289 CIDPIRCEEPYL-----RISDNRCMCPAENPGCRDQP 320
      | : | :| | | | | :| :| | | :|
Db      1520 CL----CKEGYTGDFGTCTDLDECSNENLNLG--GNGQCLNAP 1555

```

RESULT 15

A55567

fibrillin I - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002

C;Accession: A55567

R;Tilstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.

Genomics 23, 480-485, 1994

A;Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to bovine chromosome 10.

A;Reference number: A55567; MUID:95137597; PMID:7835900

A;Accession: A55567

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2871 <TIL>

A;Cross-references: GB:L28748; NID:g508427; PIDN:AAA74122.1; PID:g508428

C;Superfamily: fibrillin 1; EGF homology
F;1201-1236/Domain: EGF homology <EGF>

Query Match 21.7%; Score 522.5; DB 2; Length 2871;
Best Local Similarity 29.9%; Pred. No. 1.2e-26;
Matches 120; Conservative 45; Mismatches 124; Indels 113; Gaps 16;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      :| :|| || : | ||||| | : | | ||| | : | : : | :
Db      1054 RCDSGFALDSEERNCTDIDECRISPDLC-GRGQCVNTPGDFEC--KCDEGYESGF----- 1105

Qy      61 TPYSGPYPAAPPLSAPNYPTISR----PLICRFGYQMDSE-----NQ 99
      : | | | | | || :| | : :
Db      1106 -----MMMKNCMDIDECQRDPLLCRGGVCLNTEGSYRCECPPGHQLAPNISA 1152

Qy      100 CVDVDECATDSHQCNPTQICINTEGGYTCSTDGYWLLEGQ--CLDIDECRY--GYCQQL 155
      |:|:| | :| | | | :| | | | :| | : |:| | | | | | | :
Db      1153 CIDINECELSAHL- PHGRCVNLIGKYQCACNPGYHSTPDRLFCDVIDECSIMNGGCETF 1211

Qy      156 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENP----- 191
      | | ||| |:| ||| | | ||| |:| | :| |
Db      1212 CTNSEGSYECSCQPGFALMPDQRSTDI DEC-EDNPNICDGGQCTNIPGEYRCLCYDGM 1270

Qy      192 -----CVQ-----TCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSE 230
      || | | | | | | | | | : : |:|:| |
Db      1271 ASEDMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA 1330

Qy      231 FLCQHE--CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFK 288
      | | | | |:| ||| |:| | | | |:| | : | | | :| :
Db      1331 HNCDRHAVCTNTAGSFKCSCSPGWI--GDGIKCTDLDECSNGTHMCSQHADCKNTMGSYR 1388

Qy      289 CIDPIRCEEPYL-----RISDNRCMCPAENPGCRDQP 320
      |: | | | | | | | | | | | | |
Db      1389 CL----CKEGYTGDGFTCTDLDECSENLNLC--GNGQCLNAP 1424
```

Search completed: January 9, 2004, 12:34:54
Job time : 17.0264 secs

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:21:36 ; Search time 9.71297 Seconds
(without alignments)
2048.013 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|--------|---------------|--------|----|------------|--------------------|
| 1 | 2407 | 100.0 | 448 | 1 | FBL5_HUMAN | Q9ubx5 homo sapien |
| 2 | 2303 | 95.7 | 448 | 1 | FBL5_RAT | Q9wvh8 rattus norv |
| 3 | 2302 | 95.6 | 448 | 1 | FBL5_MOUSE | Q9wvh9 mus musculu |
| 4 | 1276.5 | 53.0 | 443 | 1 | FBL4_CRIGR | O55058 cricetulus |
| 5 | 1276.5 | 53.0 | 443 | 1 | FBL4_HUMAN | O95967 homo sapien |
| 6 | 1272.5 | 52.9 | 443 | 1 | FBL4_MOUSE | Q9wvj9 mus musculu |
| 7 | 1108.5 | 46.1 | 493 | 1 | FBL3_RAT | O35568 rattus norv |
| 8 | 1093.5 | 45.4 | 493 | 1 | FBL3_HUMAN | Q12805 homo sapien |
| 9 | 729.5 | 30.3 | 1221 | 1 | FBL2_MOUSE | P37889 mus musculu |
| 10 | 721 | 30.0 | 598 | 1 | FBL1_CERAE | Q8mjj9 cercopithec |
| 11 | 713 | 29.6 | 704 | 1 | FBL1_CHICK | O73775 gallus gall |
| 12 | 701.5 | 29.1 | 1184 | 1 | FBL2_HUMAN | P98095 homo sapien |
| 13 | 700 | 29.1 | 703 | 1 | FBL1_HUMAN | P23142 homo sapien |
| 14 | 699 | 29.0 | 705 | 1 | FBL1_MOUSE | Q08879 mus musculu |
| 15 | 629.5 | 26.2 | 681 | 1 | FBL1_BRARE | O42182 brachydanio |
| 16 | 574 | 23.8 | 798 | 1 | FBL1_CAEEL | O77469 caenorhabdi |
| 17 | 539 | 22.4 | 1394 | 1 | LTBS_HUMAN | P22064 homo sapien |

| | | | | | | | |
|----|-------|------|------|---|------------|--------|-------------|
| 18 | 539 | 22.4 | 1595 | 1 | LTBL_HUMAN | Q14766 | homo sapien |
| 19 | 523.5 | 21.7 | 2871 | 1 | FBN1_HUMAN | P35555 | homo sapien |
| 20 | 522.5 | 21.7 | 2871 | 1 | FBN1_BOVIN | P98133 | bos taurus |
| 21 | 518 | 21.5 | 1712 | 1 | LTB1_RAT | Q00918 | rattus norv |
| 22 | 516.5 | 21.5 | 2871 | 1 | FBN1_PIG | Q9tv36 | sus scrofa |
| 23 | 516 | 21.4 | 1389 | 1 | LTBS_MOUSE | Q8cg18 | mus musculu |
| 24 | 516 | 21.4 | 1713 | 1 | LTBL_MOUSE | Q8cg19 | mus musculu |
| 25 | 509.5 | 21.2 | 2871 | 1 | FBN1_MOUSE | Q61554 | mus musculu |
| 26 | 509.5 | 21.2 | 2907 | 1 | FBN2_MOUSE | Q61555 | mus musculu |
| 27 | 508.5 | 21.1 | 2911 | 1 | FBN2_HUMAN | P35556 | homo sapien |
| 28 | 455 | 18.9 | 956 | 1 | MTN2_HUMAN | O00339 | homo sapien |
| 29 | 431 | 17.9 | 956 | 1 | MTN2_MOUSE | O08746 | mus musculu |
| 30 | 421 | 17.5 | 931 | 1 | EMR1_MOUSE | Q61549 | mus musculu |
| 31 | 392 | 16.3 | 886 | 1 | EMR1_HUMAN | Q14246 | homo sapien |
| 32 | 375 | 15.6 | 2470 | 1 | NTC2_MOUSE | O35516 | mus musculu |
| 33 | 372 | 15.5 | 810 | 1 | NEL1_HUMAN | Q92832 | homo sapien |
| 34 | 372 | 15.5 | 816 | 1 | NEL2_MOUSE | Q61220 | mus musculu |
| 35 | 369 | 15.3 | 2471 | 1 | NTC2_HUMAN | Q04721 | homo sapien |
| 36 | 367 | 15.2 | 2471 | 1 | NTC2_RAT | Q9qw30 | rattus norv |
| 37 | 364 | 15.1 | 810 | 1 | NEL1_RAT | Q62919 | rattus norv |
| 38 | 361.5 | 15.0 | 816 | 1 | NEL2_HUMAN | Q99435 | homo sapien |
| 39 | 357.5 | 14.9 | 816 | 1 | NEL2_RAT | Q62918 | rattus norv |
| 40 | 355.5 | 14.8 | 816 | 1 | NEL_CHICK | Q90827 | gallus gall |
| 41 | 353.5 | 14.7 | 1964 | 1 | NTC4_MOUSE | P31695 | mus musculu |
| 42 | 351.5 | 14.6 | 2437 | 1 | NTC1_BRARE | P46530 | brachydanio |
| 43 | 350.5 | 14.6 | 652 | 1 | CD93_HUMAN | Q9npy3 | homo sapien |
| 44 | 348.5 | 14.5 | 2703 | 1 | NOTC_DROME | P07207 | drosophila |
| 45 | 347 | 14.4 | 644 | 1 | CD93_MOUSE | O89103 | mus musculu |

ALIGNMENTS

RESULT 1

FBL5_HUMAN

ID FBL5_HUMAN STANDARD; PRT; 448 AA.
AC Q9UBX5; O75966;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE EGF-like protein) (Dance) (Urine p50 protein) (UP50).
GN FBLN5 OR DANCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RA Kostka G.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357779; PubMed=10428823;
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,

RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
 RT "DANCE, a novel secreted RGD protein expressed in developing,
 RT atherosclerotic, and balloon-injured arteries.";
 RL J. Biol. Chem. 274:22476-22483(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urine;
 RA Zemel R., Sholto O., Shaul Y.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
 CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
 CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
 CC DEVELOPMENT AND REMODELING.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN HEART, OVARY, AND
 CC COLON BUT ALSO IN KIDNEY, PANCREAS, TESTIS, LUNG, AND PLACENTA.
 CC NOT DETECTABLE IN BRAIN, LIVER, THYMUS, PROSTATE, OR PERIPHERAL
 CC BLOOD LEUKOCYTES.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ133490; CAB38568.1; -.
 DR EMBL; AF112152; AAD41768.1; -.
 DR EMBL; AF093118; AAC62107.1; -.
 DR HSSP; P00736; 1APQ.
 DR Genew; HGNC:3602; FBLN5.
 DR MIM; 604580; -.
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005178; F:integrin binding activity; TAS.
 DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
 KW Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 448 FIBULIN-5.
 FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

| | | | | |
|----|----------|---------|-----------|--|
| FT | DOMAIN | 288 | 333 | EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL). |
| FT | SITE | 54 | 56 | CELL ATTACHMENT SITE (POTENTIAL). |
| FT | DISULFID | 131 | 144 | BY SIMILARITY. |
| FT | DISULFID | 138 | 153 | BY SIMILARITY. |
| FT | DISULFID | 155 | 166 | BY SIMILARITY. |
| FT | DISULFID | 172 | 181 | BY SIMILARITY. |
| FT | DISULFID | 177 | 190 | BY SIMILARITY. |
| FT | DISULFID | 192 | 205 | BY SIMILARITY. |
| FT | DISULFID | 211 | 221 | BY SIMILARITY. |
| FT | DISULFID | 217 | 230 | BY SIMILARITY. |
| FT | DISULFID | 232 | 245 | BY SIMILARITY. |
| FT | DISULFID | 251 | 262 | BY SIMILARITY. |
| FT | DISULFID | 258 | 271 | BY SIMILARITY. |
| FT | DISULFID | 273 | 286 | BY SIMILARITY. |
| FT | DISULFID | 292 | 305 | BY SIMILARITY. |
| FT | DISULFID | 299 | 314 | BY SIMILARITY. |
| FT | DISULFID | 320 | 332 | BY SIMILARITY. |
| FT | CARBOHYD | 283 | 283 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 296 | 296 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CONFLICT | 69 | 70 | IP -> HS (IN REF. 3). |
| FT | CONFLICT | 147 | 148 | TE -> MK (IN REF. 3). |
| SQ | SEQUENCE | 448 AA; | 50180 MW; | 19FCA51FDA328003 CRC64; |

Query Match 100.0%; Score 2407; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.1e-171;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | | | |
|----|-----|--|-------------------------------------|--------------------|-------------------|
| Qy | 1 | QCTNGFDLDRQSGQCLDI | DECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRG | PYSPNPYS | 60 |
| | | | | | |
| Db | 26 | QCTNGFDLDRQSGQCLDI | DECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRG | PYSPNPYS | 85 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD | ESNQCVDVDECATDSHQCNP | TQICICI | 120 |
| | | | | | |
| Db | 86 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD | ESNQCVDVDECATDSHQCNP | TQICICI | 145 |
| Qy | 121 | NTEGGYTCSC | TDGYWLLEGQCLDI | DECYGYCQQLCANVPGSY | SCTCNPGFTLNEDGRSC |
| | | | | | |
| Db | 146 | NTEGGYTCSC | TDGYWLLEGQCLDI | DECYGYCQQLCANVPGSY | SCTCNPGFTLNEDGRSC |
| Qy | 181 | QDVNECATENPCVQTCVNTYGSFICRCDPGYE | LEEDGVHCSDMDECSFSEFLCQHECVNQ | | 240 |
| | | | | | |
| Db | 206 | QDVNECATENPCVQTCVNTYGSFICRCDPGYE | LEEDGVHCSDMDECSFSEFLCQHECVNQ | | 265 |
| Qy | 241 | PGTYFCSCPPGYILLDDNRSCDINECEHRNHTCNLQQT | CYNLQGGFKCIDPIRCEEPYL | | 300 |
| | | | | | |
| Db | 266 | PGTYFCSCPPGYILLDDNRSCDINECEHRNHTCNLQQT | CYNLQGGFKCIDPIRCEEPYL | | 325 |
| Qy | 301 | RISDNRCMCPAENPGCRDQPF | TILYRDMDVVSGRSVPADIFQM | QATTRYPGAYYIFQIKS | 360 |
| | | | | | |
| Db | 326 | RISDNRCMCPAENPGCRDQPF | TILYRDMDVVSGRSVPADIFQM | QATTRYPGAYYIFQIKS | 385 |
| Qy | 361 | GNEGREFYMRQTGPISATLVMTRPIKGP | REIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | | 420 |
| | | | | | |
| Db | 386 | GNEGREFYMRQTGPISATLVMTRPIKGP | REIQLDLEMITVNTVINFRGSSVIRLRIYVSQ | | 445 |
| Qy | 421 | YPF | | | 423 |
| | | | | | |

RESULT 2

FBL5_RAT

ID FBL5_RAT STANDARD; PRT; 448 AA.
AC Q9WVH8; Q9R284;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing
DE protein) (EVEC).
GN FBLN5 OR DANCE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357779; PubMed=10428823;
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT "DANCE, a novel secreted RGD protein expressed in developing,
RT atherosclerotic, and balloon-injured arteries.";
RL J. Biol. Chem. 274:22476-22483(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99278197; PubMed=10347091;
RA Kowal R.C., Richardson J.A., Miano J.M., Olson E.N.;
RT "EVEC, a novel epidermal growth factor-like repeat-containing protein
RT upregulated in embryonic and diseased adult vasculature.";
RL Circ. Res. 84:1166-1176(1999).
CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
CC DEVELOPMENT AND REMODELING.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF112153; AAD41769.1; -.
DR EMBL; AF137350; AAD25101.1; -.
DR HSSP; P00736; 1APQ.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 4.

DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
 KW Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 448 FIBULIN-5.
 FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 288 333 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT SITE 54 56 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 131 144 BY SIMILARITY.
 FT DISULFID 138 153 BY SIMILARITY.
 FT DISULFID 155 166 BY SIMILARITY.
 FT DISULFID 172 181 BY SIMILARITY.
 FT DISULFID 177 190 BY SIMILARITY.
 FT DISULFID 192 205 BY SIMILARITY.
 FT DISULFID 211 221 BY SIMILARITY.
 FT DISULFID 217 230 BY SIMILARITY.
 FT DISULFID 232 245 BY SIMILARITY.
 FT DISULFID 251 262 BY SIMILARITY.
 FT DISULFID 258 271 BY SIMILARITY.
 FT DISULFID 273 286 BY SIMILARITY.
 FT DISULFID 292 305 BY SIMILARITY.
 FT DISULFID 299 314 BY SIMILARITY.
 FT DISULFID 320 332 BY SIMILARITY.
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 238 238 L -> P (IN REF. 2).
 SQ SEQUENCE 448 AA; 50160 MW; E6BC68F7BF14B714 CRC64; .

Query Match 95.7%; Score 2303; DB 1; Length 448;
 Best Local Similarity 94.8%; Pred. No. 5.5e-164;
 Matches 401; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
 |||||||||:|||||||||||||||||||||||||||||||||||||||
 Db 26 QCTNGFDLDRQTGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 85
 QY 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 120
 | |||||||||: | |||||||||: ||||||| |||||||||||||||||
 Db 86 TSYSGPYPAAPPVPASNYPTISRPLVCRFGYQMDEGNQCVDVDECATDSHCNPTQICI 145
 QY 121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
 |||||||||||||||||||||||||||||||||||||||||||||: |||||
 Db 146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNDDGRSC 205
 QY 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
 ||||| |||||||||: ||||||||| ||||||||| |||||||||
 Db 206 QDVNECETENPCVQTCVNTYGSFICRCDPGYELEEDGIHCSDMDECSFSEFLCQHECVNQ 265
 QY 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQGGFKCIDPIRCEEPYL 300

```

      ||:|||||||:|:||||||| ||||| |||||
Db      266 PGSYFCSCPPGYVLLEDNRSCQDINECEHRNHTCTPLQTCYNLQGGFKCIDPIVCEEPYL 325
Qy      301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      | ||||| |||||:||||||| ||||| |||||
Db      326 LIGDNRCMCPAENTGCRDQPFITILFRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385
Qy      361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      ||||| |||||:||||||| ||||| |||||
Db      386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445
Qy      421 YPF 423
      |||
Db      446 YPF 448

```

RESULT 3

FBL5_MOUSE

```

ID   FBL5_MOUSE          STANDARD;          PRT;          448 AA.
AC   Q9WVH9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE   EGF-like protein) (Dance).
GN   FBLN5 OR DANCE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99357779; PubMed=10428823;
RA   Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA   Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA   Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT   "DANCE, a novel secreted RGD protein expressed in developing,
RT   atherosclerotic, and balloon-injured arteries.";
RL   J. Biol. Chem. 274:22476-22483(1999).
CC   -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
CC   INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
CC   LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
CC   DEVELOPMENT AND REMODELING.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the fibulin family.
CC   -!- SIMILARITY: Contains 6 EGF-like domains.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; AF112151; AAD41767.1; -.
DR   HSSP; P00736; 1APQ.

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DR MGD; MGI:1346091; Fbln5.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
 KW Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 448 FIBULIN-5.
 FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 288 333 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT SITE 54 56 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 131 144 BY SIMILARITY.
 FT DISULFID 138 153 BY SIMILARITY.
 FT DISULFID 155 166 BY SIMILARITY.
 FT DISULFID 172 181 BY SIMILARITY.
 FT DISULFID 177 190 BY SIMILARITY.
 FT DISULFID 192 205 BY SIMILARITY.
 FT DISULFID 211 221 BY SIMILARITY.
 FT DISULFID 217 230 BY SIMILARITY.
 FT DISULFID 232 245 BY SIMILARITY.
 FT DISULFID 251 262 BY SIMILARITY.
 FT DISULFID 258 271 BY SIMILARITY.
 FT DISULFID 273 286 BY SIMILARITY.
 FT DISULFID 292 305 BY SIMILARITY.
 FT DISULFID 299 314 BY SIMILARITY.
 FT DISULFID 320 332 BY SIMILARITY.
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 448 AA; 50193 MW; F15CC70CCFBFDC97 CRC64;

Query Match 95.6%; Score 2302; DB 1; Length 448;
 Best Local Similarity 94.8%; Pred. No. 6.6e-164;
 Matches 401; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 85
 Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI 120
 | |||||||||: | |||||||: ||||||| ||||||||||||||||
 Db 86 TSYSGPYPAAPPVPASNYPTISRPLVCRFGYQMDEGNQCVDVDECATDSHQCNPQTQICI 145
 Qy 121 NTEGGYTCSTDGYWLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
 ||||||||||||||||||||||||||||||||||||||||||||: |||||
 Db 146 NTEGGYTCSTDGYWLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNDDGRSC 205
 Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240


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ID FBL4 HUMAN STANDARD; PRT; 443 AA.
AC O95967; O75967;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE EGF-containing fibulin-like extracellular matrix protein 2 precursor
DE (Fibulin-4) (FIBL-4) (UPH1 protein).
GN EFEMP2 OR FBLN4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RX MEDLINE=20068041; PubMed=10601734;
RA Giltay R., Timpl R., Kostka G.;
RT "Sequence, recombinant expression and tissue localization of two novel
RT extracellular matrix proteins, fibulin-3 and fibulin-4.";
RL Matrix Biol. 18:469-480(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Zemel R., Shaul Y.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20435063; PubMed=10982184;
RA Katsanis N., Venable S., Smith J.R., Lupski J.R.;
RT "Isolation of a paralog of the Doyme honeycomb retinal dystrophy gene
RT from the multiple retinopathy critical region on 11q13.";
RL Hum. Genet. 106:66-72(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC -----
 DR EMBL; AJ132819; CAA10791.2; -.
 DR EMBL; AF093119; AAC62108.1; -.
 DR EMBL; AF109121; AAF65188.1; -.
 DR EMBL; BC010456; AAH10456.1; -.
 DR HSSP; P35555; 1EMN.
 DR Genew; HGNC:3219; EFEMP2.
 DR MIM; 604633; -.
 DR GO; GO:0005604; C:basement membrane; TAS.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001491; Thrbomoduln.
 DR Pfam; PF00008; EGF; 4.
 DR PRINTS; PR00907; THRMBOMODULN.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
 FT MATRIX PROTEIN 2.
 FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

| | | | | |
|----|----------|---------|-----------|--|
| FT | DOMAIN | 243 | 282 | EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 283 | 328 | EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 127 | 140 | BY SIMILARITY. |
| FT | DISULFID | 134 | 149 | BY SIMILARITY. |
| FT | DISULFID | 151 | 162 | BY SIMILARITY. |
| FT | DISULFID | 168 | 177 | BY SIMILARITY. |
| FT | DISULFID | 173 | 186 | BY SIMILARITY. |
| FT | DISULFID | 188 | 201 | BY SIMILARITY. |
| FT | DISULFID | 207 | 217 | BY SIMILARITY. |
| FT | DISULFID | 213 | 226 | BY SIMILARITY. |
| FT | DISULFID | 228 | 241 | BY SIMILARITY. |
| FT | DISULFID | 247 | 258 | BY SIMILARITY. |
| FT | DISULFID | 254 | 267 | BY SIMILARITY. |
| FT | DISULFID | 269 | 281 | BY SIMILARITY. |
| FT | DISULFID | 287 | 300 | BY SIMILARITY. |
| FT | DISULFID | 294 | 309 | BY SIMILARITY. |
| FT | DISULFID | 315 | 327 | BY SIMILARITY. |
| FT | CARBOHYD | 198 | 198 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 394 | 394 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CONFLICT | 5 | 5 | A -> T (IN REF. 1). |
| FT | CONFLICT | 44 | 51 | EWDPDSQH -> TQTAN (IN REF. 2). |
| FT | CONFLICT | 103 | 111 | AQHPNPCPP -> VNTQPLPT (IN REF. 2). |
| FT | CONFLICT | 294 | 294 | C -> W (IN REF. 2). |
| FT | CONFLICT | 354 | 356 | RSV -> AER (IN REF. 2). |
| FT | CONFLICT | 355 | 355 | S -> R (IN REF. 3). |
| SQ | SEQUENCE | 443 AA; | 49391 MW; | 9E9AC2393780D3B8 CRC64; |

| | | | | | | | |
|----|-----|--------------------|-----------------|--------------|----------------------|------------------------|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDI | DECR | T | PEACRGDMMCVNQNGGYLCI | PRTNPVYRGPYSNPYS | 60 |
| | | : | : | : | : | : | |
| Db | 38 | ECTDGYEWD | PDSQHCRDVNECL | T | PEACKGEMKCINHYGGYLCL | PRSA | 93 |
| | | : | : | : | : | : | |
| Qy | 61 | TPYSGPY | PAAAPPLSAPNYPTI | SRPLI | CRFGYQMD | ESNQ | 120 |
| | | : | : | : | : | : | |
| Db | 94 | --- | EGP-PPP | VPPAQHPN | ----- | PCPPGYEPDDQD | 141 |
| | | : | : | : | : | : | |
| Qy | 121 | NTEGGYT | CSC | TDGYWL | LEGQCLDI | DECRYGYCQQL | 180 |
| | | : | : | : | : | : | |
| Db | 142 | NLP | GSYQCTCPDGYRKIG | PE | CV | DI | 201 |
| | | : | : | : | : | : | |
| Qy | 181 | QDVNECATEN | PCVQTCVNTYGSFI | CRC | DPGYE | LEEDGVH | 240 |
| | | : | : | : | : | : | |
| Db | 202 | VDVNECDM | GAPCEQRCFNSYGT | F | LCRCHQGYEL | HRDGFSCSDI | 261 |
| | | : | : | : | : | : | |
| Qy | 241 | PGTYFC | SCPPGYI | LLDDNR | SCQDINECEHRNHT | CNLQQTCYNLQGGFKC | 300 |
| | | : | : | : | : | : | |
| Db | 262 | PGRFSCH | CPQGYQLL-ATRL | CQDI | DECESGAHQ | CSEAQTCVNFHGGYRC | 320 |
| | | : | : | : | : | : | |
| Qy | 301 | RISDNRC | MC | PAENPGCRDQ | PFTILYRDM | VVSGRSVPADIFQM | 360 |
| | | : | : | : | : | : | |
| Db | 321 | QVSEN | RCLCPASNPLCREQ | PSSIVHRYMTIT | SERSVPADVFQI | QATSVYPGAYNAFQIRA | 380 |
| | | : | : | : | : | : | |
| Qy | 361 | GNEGREFY | MRQTGPISATL | VMTRPIKGP | PREIQLDLEMIT | TVNTVINFRGSSVIRLRIYVSQ | 420 |
| | | : | : | : | : | : | |

Db 381 GNSQGDFYIRQINNVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGA 440

QY 421 YPF 423

Db 441 YTF 443

RESULT 6

FBL4_MOUSE

ID FBL4_MOUSE STANDARD; PRT; 443 AA.

AC Q9WVJ9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE EGF-containing fibulin-like extracellular matrix protein 2 precursor

DE (Fibulin-4) (FIBL-4) (Mutant p53 binding protein 1).

GN EFEMP2 OR FBLN4 OR MBP1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RX MEDLINE=99308589; PubMed=10380882;

RA Gallagher W.M., Argentini M., Sierra V., Bracco L., Debussche L.,

RA Conseiller E.;

RT "MBP1: a novel mutant p53-specific protein partner with oncogenic

RT properties.";

RL Oncogene 18:3608-3616(1999).

CC -!- SUBUNIT: BINDS PREFERENTIALLY TO P53 MUTANTS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the fibulin family.

CC -!- SIMILARITY: Contains 6 EGF-like domains.

CC -----

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CC the European Bioinformatics Institute. There are no restrictions on its

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF104223; AAD45219.1; -.

DR HSSP; P00736; 1APQ.

DR MGD; MGI:1891209; Efemp2.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR001491; Thrbomoduln.

DR Pfam; PF00008; EGF; 4.

DR PRINTS; PR00907; THRMBOMODULN.

DR SMART; SM00179; EGF_CA; 4.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF_1; FALSE_NEG.

DR PROSITE; PS01186; EGF_2; 4.

DR PROSITE; PS01187; EGF_CA; 6.

KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
 FT MATRIX PROTEIN 2.
 FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 243 282 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 283 328 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 127 140 BY SIMILARITY.
 FT DISULFID 134 149 BY SIMILARITY.
 FT DISULFID 151 162 BY SIMILARITY.
 FT DISULFID 168 177 BY SIMILARITY.
 FT DISULFID 173 186 BY SIMILARITY.
 FT DISULFID 188 201 BY SIMILARITY.
 FT DISULFID 207 217 BY SIMILARITY.
 FT DISULFID 213 226 BY SIMILARITY.
 FT DISULFID 228 241 BY SIMILARITY.
 FT DISULFID 247 258 BY SIMILARITY.
 FT DISULFID 254 267 BY SIMILARITY.
 FT DISULFID 269 281 BY SIMILARITY.
 FT DISULFID 287 300 BY SIMILARITY.
 FT DISULFID 294 309 BY SIMILARITY.
 FT DISULFID 315 327 BY SIMILARITY.
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 443 AA; 49425 MW; 4969C0328A23DD88 CRC64;

Query Match 52.9%; Score 1272.5; DB 1; Length 443;
 Best Local Similarity 52.0%; Pred. No. 1.7e-87;
 Matches 220; Conservative 65; Mismatches 121; Indels 17; Gaps 3;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 60
 :||:|::| | | |::|| |||||:|:| |:| |||||:|:| | :
 Db 38 ECTDGYEWDADSQHCRDVNECLTIPEACKGEMKGINHYGGYLCLPRSAAVISDLHG---- 93
 Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICI 120
 || | || :| | ||: || ||||| | | |:| |
 Db 94 ---EGPPPPAA-----HAQQPNPCPGYEPDEQESCVDVDECTQALHDCRPSQDCH 141
 Qy 121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
 | | | |:| || | : |:| ||||| || | |:| |: | | | | : |||
 Db 142 NLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSC 201
 Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
 |||| | | | |:| |:| |:| |:| || | || |:| |: | : |:| |: |||:
 Db 202 VDVNECDMGAPCEQRCFNSYGTFLCRCNQGYELHRDGFSCSDIDECGYSSYLCQYRCVNE 261
 Qy 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
 || : | | | | | | | |||:| | | | | | | |:| |:| | | | | : |||:
 Db 262 PGRFSCHCPQGYQLL-ATRLCQDIDECETGAHQCEAQTVCNHFHGGYRCVDTNRCVEPYV 320
 Qy 301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKS 360
 ::||| |:| | | | |:| |:| | : | | |||||:|:| |:| | ||| | |:|:
 Db 321 QVSDNRCLCPASNPLCREQPSSIVHRYMSITERSVPAADVFIQATSVPAYNAFQIRS 380

| | | | | |
|----|----------|---------|-----------|---|
| FT | SIGNAL | 1 | 17 | POTENTIAL. |
| FT | CHAIN | 18 | 493 | EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR |
| FT | | | | MATRIX PROTEIN 1. |
| FT | DOMAIN | 26 | 71 | EGF-LIKE 1, DIVERGENT. |
| FT | DOMAIN | 173 | 213 | EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 214 | 253 | EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 254 | 293 | EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 294 | 333 | EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 334 | 378 | EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 177 | 190 | BY SIMILARITY. |
| FT | DISULFID | 184 | 199 | BY SIMILARITY. |
| FT | DISULFID | 201 | 212 | BY SIMILARITY. |
| FT | DISULFID | 218 | 228 | BY SIMILARITY. |
| FT | DISULFID | 224 | 237 | BY SIMILARITY. |
| FT | DISULFID | 239 | 252 | BY SIMILARITY. |
| FT | DISULFID | 258 | 268 | BY SIMILARITY. |
| FT | DISULFID | 264 | 277 | BY SIMILARITY. |
| FT | DISULFID | 279 | 292 | BY SIMILARITY. |
| FT | DISULFID | 298 | 309 | BY SIMILARITY. |
| FT | DISULFID | 305 | 318 | BY SIMILARITY. |
| FT | DISULFID | 320 | 332 | BY SIMILARITY. |
| FT | DISULFID | 338 | 350 | BY SIMILARITY. |
| FT | DISULFID | 344 | 359 | BY SIMILARITY. |
| FT | DISULFID | 365 | 377 | BY SIMILARITY. |
| SQ | SEQUENCE | 493 AA; | 54596 MW; | 22DAFD70BACF1CA5 CRC64; |

Query Match 46.1%; Score 1108.5; DB 1; Length 493;
 Best Local Similarity 43.6%; Pred. No. 2.7e-75;
 Matches 204; Conservative 68; Mismatches 149; Indels 47; Gaps 5;

| | | | |
|----|-----|--|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS | 60 |
| | | : : : : : : | |
| Db | 28 | QCTDGYEWDVPVRQQCKDIDECDIVPDAKGGMKCVNHYGGYLCPLPKTAQIIVNNEQPQQE | 87 |
| Qy | 61 | TPYS-----GYPYAAAPPLSAPNYPT----- | 81 |
| | | : : : : : : : : | |
| Db | 88 | TPAAEASSGAATGTIAARSMATSGVIPGGGFIASATAVAGPEVQTGRNNFVIRRNPADPQ | 147 |
| Qy | 82 | -----ISRPLICRFGYQMDESNQCVDDVDECATDSHQCNPTQICINTEGGYTCSCDTGYNL | 136 |
| | | : : : : : : : : : | |
| Db | 148 | RIPSNPSHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRLDQVCINLRGSFTCHCLPGYQK | 207 |
| Qy | 137 | LEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQT | 195 |
| | | : : : : : : | |
| Db | 208 | RGEQCVDIDECSPVPPYCHQGCVNTPGSFYCQCNPQFQLAANNYTCVDINECDASNQCAQQ | 267 |
| Qy | 196 | CVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILL | 255 |
| | | : : : : : : : : : : : | |
| Db | 268 | CYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCPQGYQVV | 327 |
| Qy | 256 | DDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPG | 315 |
| | | : : : : : : : : : : | |
| Db | 328 | -RSRTCQDINECETTNE-CREDEMWNHYHGGFRFCYPQNPCQDPYVLTSENRCVCPVSNTM | 385 |
| Qy | 316 | CRDQPFITILYRDMDVVSGRSPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPI | 375 |
| | | : : : : : : : : | |
| Db | 386 | CRDVPQSI VYKYMNI RSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGFEYLRQTSPV | 445 |

Qy 376 SATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
 || ||: : : |||| : |||:|:|:| || |||:| | | : |
 Db 446 SAMLVLVKSLTGPREHIVGLEMLTVSSIGTFRTSSVLRLTIIVGPF SF 493

RESULT 8

FBL3_HUMAN

ID FBL3_HUMAN STANDARD; PRT; 493 AA.
 AC Q12805;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE EGF-containing fibulin-like extracellular matrix protein 1 precursor
 DE (Fibulin-3) (FIBL-3) (Fibrillin-like protein) (Extracellular protein
 DE S1-5).
 GN EFEMP1 OR FBLN3 OR FBNL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND POSSIBLE ALTERNATIVE SPLICING.
 RC TISSUE=Skin;
 RX MEDLINE=95097983; PubMed=7799918;
 RA Lecka-Czernik B., Lumpkin C.K. Jr., Goldstein S.;
 RT "An overexpressed gene transcript in senescent and quiescent human
 RT fibroblasts encoding a novel protein in the epidermal growth factor-
 RT like repeat family stimulates DNA synthesis.";
 RL Mol. Cell. Biol. 15:120-128(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97001163; PubMed=8812496;
 RA Ikegawa S., Toda T., Okui K., Nakamura Y.;
 RT "Structure and chromosomal assignment of the human S1-5 gene (FBNL)
 RT that is highly homologous to fibrillin.";
 RL Genomics 35:590-592(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20068041; PubMed=10601734;
 RA Giltay R., Timpl R., Kostka G.;
 RT "Sequence, recombinant expression and tissue localization of two novel
 RT extracellular matrix proteins, fibulin-3 and fibulin-4.";
 RL Matrix Biol. 18:469-480(1999).
 RN [4]
 RP VARIANT DHRD/MLVT TRP-345, AND VARIANT PHE-220.
 RX MEDLINE=99295941; PubMed=10369267;
 RA Stone E.M., Lotery A.J., Munier F.L., Heon E., Piguet B., Guymer R.H.,
 RA Vandenburg K., Cousin P., Nishimura D., Swiderski R.E., Silvestri G.,
 RA Mackey D.A., Hagerman G.S., Bird A.C., Sheffield V.C.,
 RA Schorderet D.F.;
 RT "A single EFEMP1 mutation associated with both malattia Leventinese
 RT and Doyme honeycomb retinal dystrophy.";
 RL Nat. Genet. 22:199-202(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;

```

CC      Comment=Experimental confirmation may be lacking for some
CC      isoforms;
CC      Name=1;
CC      IsoId=Q12805-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q12805-2; Sequence=VSP_001392;
CC      Name=3;
CC      IsoId=Q12805-3; Sequence=VSP_001393;
CC      Name=4;
CC      IsoId=Q12805-4; Sequence=VSP_001394;
CC      -!- DISEASE: DEFECTS IN EFEMP1 ARE A CAUSE OF DOYNE HONEYCOMB RETINAL
CC      DYSTROPHY (DHRD) ALSO KNOWN AS MALATTIA LEVENTINESE (MLVT OR ML),
CC      AN AUTOSOMAL DOMINANT DISEASE CHARACTERIZED BY YELLOW-WHITE
CC      DEPOSITS KNOWN AS DRUSEN THAT ACCUMULATE BENEATH THE RETINAL
CC      PIGMENT EPITHELIUM.
CC      -!- SIMILARITY: Belongs to the fibulin family.
CC      -!- SIMILARITY: Contains 6 EGF-like domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U03877; AAA65590.1; -.
DR      HSSP; P35555; 1EMN.
DR      Genew; HGNC:3218; EFEMP1.
DR      MIM; 601548; -.
DR      MIM; 126600; -.
DR      GO; GO:0005578; C:extracellular matrix; TAS.
DR      GO; GO:0007601; P:vision; TAS.
DR      InterPro; IPR000152; Asx_hydroxyl.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR006209; EGF_like.
DR      Pfam; PF00008; EGF; 3.
DR      SMART; SM00179; EGF_CA; 4.
DR      PROSITE; PS00010; ASX_HYDROXYL; 4.
DR      PROSITE; PS00022; EGF_1; FALSE_NEG.
DR      PROSITE; PS01186; EGF_2; 4.
DR      PROSITE; PS01187; EGF_CA; 6.
KW      Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal;
KW      Disease mutation; Polymorphism; Alternative splicing.
FT      SIGNAL          1      17      POTENTIAL.
FT      CHAIN           18     493      EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT                                     MATRIX PROTEIN 1.
FT      DOMAIN          26      71      EGF-LIKE 1, DIVERGENT.
FT      DOMAIN          173     213      EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT      DOMAIN          214     253      EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT      DOMAIN          254     293      EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT      DOMAIN          294     333      EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT      DOMAIN          334     378      EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT      DISULFID        177     190      BY SIMILARITY.
FT      DISULFID        184     199      BY SIMILARITY.
FT      DISULFID        201     212      BY SIMILARITY.
FT      DISULFID        218     228      BY SIMILARITY.

```

| | | | | |
|----|----------|---------|-----------|-------------------------------------|
| FT | DISULFID | 224 | 237 | BY SIMILARITY. |
| FT | DISULFID | 239 | 252 | BY SIMILARITY. |
| FT | DISULFID | 258 | 268 | BY SIMILARITY. |
| FT | DISULFID | 264 | 277 | BY SIMILARITY. |
| FT | DISULFID | 279 | 292 | BY SIMILARITY. |
| FT | DISULFID | 298 | 309 | BY SIMILARITY. |
| FT | DISULFID | 305 | 318 | BY SIMILARITY. |
| FT | DISULFID | 320 | 332 | BY SIMILARITY. |
| FT | DISULFID | 338 | 350 | BY SIMILARITY. |
| FT | DISULFID | 344 | 359 | BY SIMILARITY. |
| FT | DISULFID | 365 | 377 | BY SIMILARITY. |
| FT | CARBOHYD | 249 | 249 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | VARSPLIC | 1 | 8 | Missing (in isoform 2). |
| FT | | | | /FTid=VSP_001392. |
| FT | VARSPLIC | 58 | 58 | Missing (in isoform 3). |
| FT | | | | /FTid=VSP_001393. |
| FT | VARSPLIC | 106 | 106 | Missing (in isoform 4). |
| FT | | | | /FTid=VSP_001394. |
| FT | VARIANT | 220 | 220 | I -> F. |
| FT | | | | /FTid=VAR_009512. |
| FT | VARIANT | 345 | 345 | R -> W (IN MVLT). |
| FT | | | | /FTid=VAR_009513. |
| SQ | SEQUENCE | 493 AA; | 54640 MW; | 128CA5ED140DF414 CRC64; |

Query Match 45.4%; Score 1093.5; DB 1; Length 493;
 Best Local Similarity 43.2%; Pred. No. 3.6e-74;
 Matches 203; Conservative 64; Mismatches 152; Indels 51; Gaps 7;

| | | | |
|----|-----|--|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVY---RGPYSN | 57 |
| | | : : : : : : : : | |
| Db | 28 | QCTDGYEWDVPVRQQCKDIDECDIVPDAKGGMKCVNHYGGYLCPLKTAQIIVNNEQPQQE | 87 |
| | | | |
| Qy | 58 | PY-----STPYSGPYPA-----APPL | 74 |
| | | | |
| Db | 88 | TQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAVAGPEMQTGRNNFVIRRNPPADPQ | 147 |
| | | | |
| Qy | 75 | SAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGY | 134 |
| | | : : : : : : | |
| Db | 148 | RIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQCPPGY | 205 |
| | | | |
| Qy | 135 | WLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCV | 193 |
| | | : : : | |
| Db | 206 | QKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQSPGFQLAANNYTCVDINECDASNQCA | 265 |
| | | | |
| Qy | 194 | QTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYI | 253 |
| | | : : : : : | |
| Db | 266 | QQCYNIIIGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCPQGYQ | 325 |
| | | | |
| Qy | 254 | LLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPLYLRISDNRCMCPAEN | 313 |
| | | : : : : : : : : : : | |
| Db | 326 | VV-RSRTCQDINECETTNE-CREDEMWNHGGFRFCYPRNPCQDPYILTPENRCVCPVSN | 383 |
| | | | |
| Qy | 314 | PGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTG | 373 |
| | | : : : : | |
| Db | 384 | AMCRELPQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEPYLRQTS | 443 |
| | | | |
| Qy | 374 | PISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF | 423 |

Db

444 PVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 493

RESULT 9

FBL2_MOUSE

ID FBL2_MOUSE STANDARD; PRT; 1221 AA.
AC P37889; Q9WUI2;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-2 precursor.
GN FBLN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-35.
RC TISSUE=Fibroblast;
RX MEDLINE=94064787; PubMed=8245130;
RA Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.;
RT "Structure and expression of fibulin-2, a novel extracellular matrix
RT protein with multiple EGF-like repeats and consensus motifs for
RT calcium binding.";
RL J. Cell Biol. 123:1269-1277(1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99337686; PubMed=10406956;
RA Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;
RT "Mouse fibulin-2 gene. Complete exon-intron organization and promoter
RT characterization.";
RL Eur. J. Biochem. 263:471-477(1999).
RN [3]
RP DEVELOPMENTAL STAGE.
RX PubMed=8850569;
RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
RT "Fibulin-1 and fibulin-2 expression during organogenesis in the
RT developing mouse embryo.";
RL Dev. Dyn. 205:348-364(1996).
RN [4]
RP BINDING TO LAMA2.
RX PubMed=10022829;
RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
RT "Binding of the G domains of laminin alpha1 and alpha2 chains and
RT perlecan to heparin, sulfatides, alpha-dystroglycan and several
RT extracellular matrix proteins.";
RL EMBO J. 18:863-870(1999).
RN [5]
RP DOWN-REGULATION BY GLUCOCORTICOIDS.
RX PubMed=11737251;
RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
RT "Glucocorticoids down-regulate the extracellular matrix proteins
RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
RL Eur. J. Haematol. 67:176-184(2001).
CC -!- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS
CC CALCIUM DEPENDENT.


```

CC  -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2.
CC  -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Comment=Additional isoforms seem to exist;
CC      Name=1;
CC      IsoId=P37889-1; Sequence=Displayed;
CC      Name=2; Synonyms=EGF3-less;
CC      IsoId=P37889-2; Sequence=VSP_001391;
CC  -!- TISSUE SPECIFICITY: Component of both basement membranes and other
CC      connective tissues.
CC  -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin
CC      family contributes to the formation of molecularly distinct
CC      extracellular matrices already during early developmental stages
CC      of a large number of tissues.
CC  -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
CC      synthesis.
CC  -!- SIMILARITY: Belongs to the fibulin family.
CC  -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC  -!- SIMILARITY: Contains 11 EGF-like domains.
CC  -----
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CC  -----
DR  EMBL; X75285; CAA53040.1; -.
DR  EMBL; AF135253; AAD34456.1; -.
DR  EMBL; AF135239; AAD34456.1; JOINED.
DR  EMBL; AF135240; AAD34456.1; JOINED.
DR  EMBL; AF135241; AAD34456.1; JOINED.
DR  EMBL; AF135242; AAD34456.1; JOINED.
DR  EMBL; AF135243; AAD34456.1; JOINED.
DR  EMBL; AF135244; AAD34456.1; JOINED.
DR  EMBL; AF135245; AAD34456.1; JOINED.
DR  EMBL; AF135246; AAD34456.1; JOINED.
DR  EMBL; AF135247; AAD34456.1; JOINED.
DR  EMBL; AF135248; AAD34456.1; JOINED.
DR  EMBL; AF135249; AAD34456.1; JOINED.
DR  EMBL; AF135250; AAD34456.1; JOINED.
DR  EMBL; AF135251; AAD34456.1; JOINED.
DR  EMBL; AF135252; AAD34456.1; JOINED.
DR  PIR; A49457; A49457.
DR  HSSP; P00736; 1APQ.
DR  MGD; MGI:95488; Fbln2.
DR  InterPro; IPR000020; Anaphylatoxin.
DR  InterPro; IPR000152; Asx_hydroxyl.
DR  InterPro; IPR001881; EGF_Ca.
DR  InterPro; IPR006209; EGF_like.
DR  Pfam; PF01821; ANATO; 2.
DR  Pfam; PF00008; EGF; 6.
DR  SMART; SM00104; ANATO; 3.
DR  SMART; SM00179; EGF_CA; 9.
DR  PROSITE; PS00010; ASX_HYDROXYL; 5.

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DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS01187; EGF_CA; 10.
 KW Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;
 KW Calcium-binding; Alternative splicing; Repeat.
 FT SIGNAL 1 26
 FT CHAIN 27 1221 FIBULIN-2.
 FT DOMAIN 27 434 N.
 FT DOMAIN 27 176 SUBDOMAIN NA (CYS-RICH).
 FT DOMAIN 177 434 SUBDOMAIN NB (CYS-FREE).
 FT DOMAIN 435 477 ANAPHYLATOXIN-LIKE 1.
 FT DOMAIN 478 510 ANAPHYLATOXIN-LIKE 2.
 FT DOMAIN 511 543 ANAPHYLATOXIN-LIKE 3.
 FT DOMAIN 594 635 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 669 708 EGF-LIKE 2.
 FT DOMAIN 709 755 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 756 800 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 801 846 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 847 894 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 895 937 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 938 979 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 980 1018 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1019 1061 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1062 1106 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1111 1221 DOMAIN III.
 FT SITE 421 423 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 435 462 BY SIMILARITY.
 FT DISULFID 436 469 BY SIMILARITY.
 FT DISULFID 449 470 BY SIMILARITY.
 FT DISULFID 479 508 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT DISULFID 511 535 BY SIMILARITY.
 FT DISULFID 512 542 BY SIMILARITY.
 FT DISULFID 525 543 BY SIMILARITY.
 FT DISULFID 598 610 BY SIMILARITY.
 FT DISULFID 606 619 BY SIMILARITY.
 FT DISULFID 621 634 BY SIMILARITY.
 FT DISULFID 673 683 BY SIMILARITY.
 FT DISULFID 679 692 BY SIMILARITY.
 FT DISULFID 694 707 BY SIMILARITY.
 FT DISULFID 713 726 BY SIMILARITY.
 FT DISULFID 720 735 BY SIMILARITY.
 FT DISULFID 742 754 BY SIMILARITY.
 FT DISULFID 805 818 BY SIMILARITY.
 FT DISULFID 812 827 BY SIMILARITY.
 FT DISULFID 833 845 BY SIMILARITY.
 FT DISULFID 899 912 BY SIMILARITY.
 FT DISULFID 906 921 BY SIMILARITY.
 FT DISULFID 923 936 BY SIMILARITY.
 FT DISULFID 942 954 BY SIMILARITY.
 FT DISULFID 950 963 BY SIMILARITY.
 FT DISULFID 965 978 BY SIMILARITY.
 FT DISULFID 984 993 BY SIMILARITY.
 FT DISULFID 989 1002 BY SIMILARITY.
 FT DISULFID 1004 1017 BY SIMILARITY.

| | | | | |
|----|----------|----------|------------|--|
| FT | DISULFID | 1023 | 1035 | BY SIMILARITY. |
| FT | DISULFID | 1031 | 1044 | BY SIMILARITY. |
| FT | DISULFID | 1046 | 1060 | BY SIMILARITY. |
| FT | DISULFID | 1066 | 1079 | BY SIMILARITY. |
| FT | DISULFID | 1073 | 1088 | BY SIMILARITY. |
| FT | DISULFID | 1093 | 1105 | BY SIMILARITY. |
| FT | CARBOHYD | 179 | 179 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 497 | 497 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 737 | 737 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 1072 | 1072 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | VARSPLIC | 709 | 755 | Missing (in isoform 2). |
| FT | | | | /FTid=VSP_001391. |
| FT | CONFLICT | 140 | 159 | HSGRKYAAGHTVHLSSCRAC -> TVAVSICWPYRPLILP |
| FT | | | | GF (IN REF. 2). |
| FT | CONFLICT | 348 | 348 | S -> L (IN REF. 2). |
| FT | CONFLICT | 507 | 507 | Q -> QQ (IN REF. 2). |
| FT | CONFLICT | 1102 | 1102 | Q -> E (IN REF. 2). |
| SQ | SEQUENCE | 1221 AA; | 131818 MW; | 87DB2A10A8FDC45F CRC64; |

Query Match 30.3%; Score 729.5; DB 1; Length 1221;
 Best Local Similarity 35.3%; Pred. No. 9e-47;
 Matches 145; Conservative 59; Mismatches 148; Indels 59; Gaps 11;

| | | | |
|----|------|---|------|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 60 |
| | | : : | |
| Db | 832 | RCMDGF-LQDPEGNCVDINECTSLLEPCRS GFSCINTVGSYTC----- | 873 |
| | | | |
| Qy | 61 | TPYSGPYAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC | 119 |
| | | | |
| Db | 874 | -----QRNPLVCGRGYHANEESGSECVDVNECETGVHRCGEGQLC | 912 |
| | | | |
| Qy | 120 | INTEGGYTCSDTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGFTLN | 174 |
| | | | |
| Db | 913 | YNLPGSYRCDCKPGFQRDAFGRTCIDVNECWVSPGRLCQHTCENTPGSYRCSAAGFLLA | 972 |
| | | | |
| Qy | 175 | EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECS-FSEFLC | 233 |
| | | | |
| Db | 973 | ADGKHCEDVNECETRR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC | 1031 |
| | | | |
| Qy | 234 | QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDP | 292 |
| | | | |
| Db | 1032 | TFRCVNVPGSYQCACPEQGYTMMANGRSCKDLDECALGTHNCSEAETCHNIQGSFRCL-R | 1090 |
| | | | |
| Qy | 293 | IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT | 346 |
| | | | |
| Db | 1091 | FDCPPNYVRVSQTKC----ERTTCQDITECQTS PARITHYQLNFQTGLLVPAHIFRIGPA | 1146 |
| | | | |
| Qy | 347 | TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM | 397 |
| | | : | |
| Db | 1147 | PAFAGDTISLTITKGNEEGYFVTRRLNAYTGVSLSQRSVLEPRDFALDVEM | 1197 |

RESULT 10
 FBL1_CERAE
 ID FBL1_CERAE STANDARD; PRT; 598 AA.
 AC Q8MJJ9;
 DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibulin-1C (Fragment).
 GN FBLN1.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A., AND INTERACTION WITH DTR.
 RX PubMed=11846885;
 RA Brooke J.S., Cha J.-H., Eidels L.;
 RT "Latent transforming growth factor beta-binding protein-3 and
 RT fibulin-1C interact with the extracellular domain of the
 RT heparin-binding EGF-like growth factor precursor.";
 RL BMC Cell Biol. 3:2-2(2002).
 CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
 CC May play a role in cell adhesion and migration along protein
 CC fibers within the extracellular matrix (ECM). Could be important
 CC for certain developmental processes and contribute to the
 CC supramolecular organization of ECM architecture, in particular to
 CC those of basement membranes. May serve to anchor the
 CC mature/soluble form of DTR to its fibers as it migrates through
 CC the extracellular matrix. The direct physical association with DTR
 CC may be useful in such tissue developmental processes as wound
 CC healing.
 CC -!- SUBUNIT: Interacts with itself and with various extracellular
 CC matrix components (By similarity). Interacts with the
 CC mature/soluble form of DTR.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains at least 2 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 9 EGF-like domains.
 CC -----
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 CC -----
 DR EMBL; AF395659; AAM90567.1; -.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF00008; EGF; 5.
 DR SMART; SM00104; ANATO; 1.
 DR SMART; SM00181; EGF; 9.
 DR SMART; SM00179; EGF_CA; 9.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 7.
 KW Glycoprotein; Extracellular matrix; Repeat; EGF-like domain;
 KW Calcium-binding.
 FT NON_TER 1 1
 FT CHAIN <1 598 FIBULIN-1C.
 FT DOMAIN <1 27 ANAPHYLATOXIN-LIKE 2.
 FT DOMAIN 28 60 ANAPHYLATOXIN-LIKE 3.
 FT DOMAIN 92 131 EGF-LIKE 1.
 FT DOMAIN 132 177 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 178 223 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 224 270 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 271 313 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 314 355 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 356 395 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 396 439 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 440 484 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 271 355 SELF-ASSOCIATION AND FN1-BINDING (BY
 FT SIMILARITY).
 FT DISULFID <1 25 BY SIMILARITY.
 FT DISULFID 7 26 BY SIMILARITY.
 FT DISULFID 28 52 BY SIMILARITY.
 FT DISULFID 29 59 BY SIMILARITY.
 FT DISULFID 42 60 BY SIMILARITY.
 FT DISULFID 96 106 BY SIMILARITY.
 FT DISULFID 102 115 BY SIMILARITY.
 FT DISULFID 117 130 BY SIMILARITY.
 FT DISULFID 136 149 BY SIMILARITY.
 FT DISULFID 143 158 BY SIMILARITY.
 FT DISULFID 164 176 BY SIMILARITY.
 FT DISULFID 182 195 BY SIMILARITY.
 FT DISULFID 189 204 BY SIMILARITY.
 FT DISULFID 210 222 BY SIMILARITY.
 FT DISULFID 228 242 BY SIMILARITY.
 FT DISULFID 257 270 BY SIMILARITY.
 FT DISULFID 275 288 BY SIMILARITY.
 FT DISULFID 282 297 BY SIMILARITY.
 FT DISULFID 299 312 BY SIMILARITY.
 FT DISULFID 318 330 BY SIMILARITY.
 FT DISULFID 326 339 BY SIMILARITY.
 FT DISULFID 341 354 BY SIMILARITY.
 FT DISULFID 360 369 BY SIMILARITY.
 FT DISULFID 365 378 BY SIMILARITY.
 FT DISULFID 380 394 BY SIMILARITY.
 FT DISULFID 400 413 BY SIMILARITY.
 FT DISULFID 409 422 BY SIMILARITY.
 FT DISULFID 424 438 BY SIMILARITY.
 FT DISULFID 444 457 BY SIMILARITY.
 FT DISULFID 451 466 BY SIMILARITY.
 FT DISULFID 471 483 BY SIMILARITY.
 FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 598 AA; 65516 MW; 849BF018DF452B02 CRC64;

Query Match 30.0%; Score 721; DB 1; Length 598;
 Best Local Similarity 35.3%; Pred. No. 1.9e-46;

Matches 155; Conservative 72; Mismatches 184; Indels 28; Gaps 15;

```
Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPR---TNPVYRGPYSNP 58
      |  |::|  :  | |||:| :  |  | :|  |  | :|  |  | :  |
Db      164 CGTGYEL-TEDNSCKDIDQCESGIHNCLPDFICQNTLGSFRCRPKLQCKNGFIQDALANC 222

Qy      59 YS-----TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHC 113
      :  |  |  |  :  |  |  |  |  |  |  |  |  |  |  |  |
Db      223 IDINECLSIVSAPCPTGHTCINTEGSYTQKNVPNCGRGYHLNEEGTRCDVNECAPPAEPC 282

Qy      114 NPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCN 168
      |::|  | :  |  | ||:  :  |::|  |  |  |  |  |  |  |  |
Db      283 GKGHRCVNSPGSFRCECKTGYIFYDGI SRMCVDVNECQRYPGRLCGHKCENTLGSYVCS 342

Qy      169 PGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECS 227
      ||  | :  |||||:|:|:|:|:|  |  |  |  |  |  |  |  |  |  |  |
Db      343 VGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECA 401

Qy      228 F--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQ 284
      :  | :  |::|  |||  ||  | :  |::|  |  |  |  |  |  |  |  |
Db      402 LPTGGHICSYRCINIPGSFQCSCPASGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQ 461

Qy      285 GGFKCIDPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPADIFQ 342
      |||:|:  |  |  | :  ||  |  |  |  |  |  |  |  | :  :  |  |  |
Db      462 GGFRCL-AFECPENYRRSAATRCERLPCHENRECSKPLRLITYYHLSFPTNIQAPAVVFR 520

Qy      343 MQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM--ITV 400
      |  ::  ||  |  |||  |  | :  |  |  | :  |:|  |  |::  |  ::|
Db      521 MGPSSAVPGDSMQLAITGNEEGFFTTRKVSPHSGVVALTKPVPEPRDLLLTVKMDLYRH 580

Qy      401 NTVINFRGSSVIRLRIYVS 419
      || :|  | :|  |::|
Db      581 GTVSSF----VAKLFIFVS 595
```

RESULT 11

FBL1_CHICK

ID FBL1_CHICK STANDARD; PRT; 704 AA.
AC O73775; O73774;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-1 precursor.
GN FBLN1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS C AND D).
RC TISSUE=Embryo;
RX MEDLINE=99120531; PubMed=9923656;
RA Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;
RT "Identification of chicken and C. elegans fibulin-1 homologs and
RT characterization of the C. elegans fibulin-1 gene.";
RL Matrix Biol. 17:635-646(1998).

```

CC  -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
CC      May play a role in cell adhesion and migration along protein
CC      fibers within the extracellular matrix (ECM). Could be important
CC      for certain developmental processes and contribute to the
CC      supramolecular organization of ECM architecture, in particular to
CC      those of basement membranes.
CC  -!- SUBUNIT: Interacts with itself and with various extracellular
CC      matrix components (By similarity).
CC  -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=D;
CC      IsoId=O73775-2; Sequence=Displayed;
CC      Name=C;
CC      IsoId=O73775-1; Sequence=VSP_007378;
CC  -!- SIMILARITY: Belongs to the fibulin family.
CC  -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC  -!- SIMILARITY: Contains 9 EGF-like domains.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF051399; AAC05387.1; -.
DR  EMBL; AF051400; AAC05388.1; -.
DR  HSSP; P00742; 1HCG.
DR  InterPro; IPR000020; Anaphylatoxin.
DR  InterPro; IPR000152; Asx_hydroxyl.
DR  InterPro; IPR001881; EGF_Ca.
DR  InterPro; IPR006209; EGF_like.
DR  Pfam; PF01821; ANATO; 2.
DR  Pfam; PF00008; EGF; 6.
DR  SMART; SM00104; ANATO; 3.
DR  SMART; SM00181; EGF; 9.
DR  SMART; SM00179; EGF_CA; 8.
DR  PROSITE; PS00010; ASX_HYDROXYL; 5.
DR  PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR  PROSITE; PS01178; ANAPHYLATOXIN_2; 2.
DR  PROSITE; PS00022; EGF_1; FALSE_NEG.
DR  PROSITE; PS01186; EGF_2; 3.
DR  PROSITE; PS01187; EGF_CA; 8.
KW  Signal; Alternative splicing; Glycoprotein; Extracellular matrix;
KW  Repeat; EGF-like domain; Calcium-binding.
FT  SIGNAL          1      25      POTENTIAL.
FT  CHAIN           26     704      FIBULIN-1.
FT  DOMAIN          33      74      ANAPHYLATOXIN-LIKE 1.
FT  DOMAIN          75     109      ANAPHYLATOXIN-LIKE 2.
FT  DOMAIN         110     142      ANAPHYLATOXIN-LIKE 3.
FT  DOMAIN         177     216      EGF-LIKE 1.
FT  DOMAIN         217     262      EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN         263     308      EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN         309     356      EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN         357     399      EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

```

| | | | | |
|----|----------|---------|-----------|---|
| FT | DOMAIN | 400 | 441 | EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 442 | 481 | EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 482 | 525 | EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 526 | 579 | EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 357 | 441 | SELF-ASSOCIATION AND FN1-BINDING (BY |
| FT | | | | SIMILARITY). |
| FT | DISULFID | 33 | 59 | BY SIMILARITY. |
| FT | DISULFID | 34 | 66 | BY SIMILARITY. |
| FT | DISULFID | 47 | 67 | BY SIMILARITY. |
| FT | DISULFID | 76 | 107 | BY SIMILARITY. |
| FT | DISULFID | 89 | 108 | BY SIMILARITY. |
| FT | DISULFID | 110 | 134 | BY SIMILARITY. |
| FT | DISULFID | 111 | 141 | BY SIMILARITY. |
| FT | DISULFID | 124 | 142 | BY SIMILARITY. |
| FT | DISULFID | 181 | 191 | BY SIMILARITY. |
| FT | DISULFID | 187 | 200 | BY SIMILARITY. |
| FT | DISULFID | 202 | 215 | BY SIMILARITY. |
| FT | DISULFID | 221 | 234 | BY SIMILARITY. |
| FT | DISULFID | 228 | 243 | BY SIMILARITY. |
| FT | DISULFID | 249 | 261 | BY SIMILARITY. |
| FT | DISULFID | 267 | 280 | BY SIMILARITY. |
| FT | DISULFID | 274 | 289 | BY SIMILARITY. |
| FT | DISULFID | 295 | 307 | BY SIMILARITY. |
| FT | DISULFID | 313 | 326 | BY SIMILARITY. |
| FT | DISULFID | 320 | 335 | BY SIMILARITY. |
| FT | DISULFID | 342 | 355 | BY SIMILARITY. |
| FT | DISULFID | 361 | 374 | BY SIMILARITY. |
| FT | DISULFID | 368 | 383 | BY SIMILARITY. |
| FT | DISULFID | 385 | 398 | BY SIMILARITY. |
| FT | DISULFID | 404 | 416 | BY SIMILARITY. |
| FT | DISULFID | 412 | 425 | BY SIMILARITY. |
| FT | DISULFID | 427 | 440 | BY SIMILARITY. |
| FT | DISULFID | 446 | 455 | BY SIMILARITY. |
| FT | DISULFID | 451 | 464 | BY SIMILARITY. |
| FT | DISULFID | 466 | 480 | BY SIMILARITY. |
| FT | DISULFID | 486 | 499 | BY SIMILARITY. |
| FT | DISULFID | 495 | 508 | BY SIMILARITY. |
| FT | DISULFID | 510 | 524 | BY SIMILARITY. |
| FT | DISULFID | 530 | 543 | BY SIMILARITY. |
| FT | DISULFID | 537 | 552 | BY SIMILARITY. |
| FT | DISULFID | 557 | 578 | BY SIMILARITY. |
| FT | CARBOHYD | 96 | 96 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 536 | 536 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 540 | 540 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | VARSPLIC | 568 | 704 | VRLEKTDITIRCIKSCRPNDEVNCLDPVHTISHTVISLPTFR |
| FT | | | | EFTRPEEIIIFLRAITPTYPANQADIIIFDITEGNLRESFDII |
| FT | | | | KRYMDGMTVGVVRQVRPIVGPFHAILKLEMNYVMGGVVSHR |
| FT | | | | NIVNVHIFVSEYWF -> RCERLPCNENKECQSLPLRITYY |
| FT | | | | HLSFPTNIQVPTDIFRMGPSNAVPGDKILLSIIISGNQEGFF |
| FT | | | | TTKKVNNHSGIVVMQRQITEPRDLLLTIQMLTRHGTVNTF |
| FT | | | | IAKLFFVFSQQL (in isoform C). |
| FT | | | | /FTid=VSP_007378. |
| SQ | SEQUENCE | 704 AA; | 78137 MW; | D47D5A30D5E42932 CRC64; |

Query Match 29.6%; Score 713; DB 1; Length 704;
 Best Local Similarity 35.1%; Pred. No. 8.8e-46;
 Matches 160; Conservative 64; Mismatches 154; Indels 78; Gaps 21;

| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGYYLCI PRTPVYRGPYSNPYS | 60 |
|----|-----|---|-----|
| Db | 294 | QCMNGFIQD-ALGNCIDINECLSTNMPCPAGQICINTDGSYTC-QRISP----- | 340 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ENQCVDDVDECATDSHQCNPTQIC | 119 |
| Db | 341 | -----SCGRGYHLNEDGTRCVDVDECSSDQPCGEHVC | 374 |
| Qy | 120 | INTEGGYTCSCTDGYW--LLEGQCLDIDECY--GYCQQLCANVPGSYSCTCNPGFTLN | 174 |
| Db | 375 | INGPGNYRCECKSGYSFSDVISRTCIDINECRYPGRLLCAHKCENTPGSYCTCTMGFKLS | 434 |
| Qy | 175 | EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELE-EGVHCSMDDECSF--SEF | 231 |
| Db | 435 | SDGRSCEDLNECES-SPCSQECANVYGSYQCYCRRGFQLSDIDIGISCEDIDECALPTGGH | 493 |
| Qy | 232 | LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI | 290 |
| Db | 494 | ICSFRCINIPGSFQCTCPSTGYRLAPNARNQDIDECVAETHNCSFNETCFNIQGGFRCL | 553 |
| Qy | 291 | DPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFTILYRDMDVVSGRSV-- | 336 |
| Db | 554 | S-LECPENYRKSGDTRVLEKTDTRICIKSCRPNVDNVCVLDPVHTISHTVISLPTFREFT | 612 |
| Qy | 337 | PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF----YMRQTGPISATLVMTRPIKGP | 388 |
| Db | 613 | PEEIIFLRAITPTYPANQADIIFDITEGNLRESFDIIKRYM--DGMTVGVVRQVRPIVGP | 670 |
| Qy | 389 | REIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF | 423 |
| Db | 671 | FHAILKLEMNYVMGGVVSHR--NIVNVHIFVSEYWF | 704 |

RESULT 12

FBL2 HUMAN

ID FBL2 HUMAN STANDARD; PRT; 1184 AA.

AC P98095;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Fibulin-2 precursor.

GN FBLN2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fibroblast;

RX MEDLINE=95104855; PubMed=7806230;

RA Zhang R.-Z., Pan T.-C., Zhang Z.-Y., Mattei M.-G., Timpl R.,

RA Chu M. -L. ;

RT "Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping
RT of the gene on human and mouse chromosomes.";

RL Genomics 22:425-430(1994) .

RN [2]

RP DEVELOPMENTAL STAGE.
RX PubMed=8737292;
RA Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;
RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the
RT early human embryo.";
RL Histochem. J. 28:109-116(1996).
CC -!- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS
CC CALCIUM DEPENDENT.
CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other
CC connective tissues. Expressed in heart, placenta and ovary.
CC -!- DEVELOPMENTAL STAGE: Widely expressed during embryonic
CC development. Primarily detected within the neuropithelium, spinal
CC ganglia and peripheral nerves.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC -!- SIMILARITY: Contains 11 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X82494; CAA57876.1; -.
DR PIR; A55184; A55184.
DR HSSP; P00736; 1APQ.
DR Genew; HGNC:3601; FBLN2.
DR MIM; 135821; -.
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR GO; GO:0005509; F:calcium ion binding activity; TAS.
DR GO; GO:0005207; F:extracellular matrix glycoprotein; TAS.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF00008; EGF; 7.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00179; EGF_CA; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01187; EGF_CA; 9.
KW Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;
KW Calcium-binding; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 1184 FIBULIN-2.
FT DOMAIN 28 444 N.
FT DOMAIN 28 177 SUBDOMAIN NA (CYS-RICH).
FT DOMAIN 178 444 SUBDOMAIN NB (CYS-FREE).

| | | | | |
|----|----------|------|---------------------------------|-------------------------------------|
| FT | DOMAIN | 445 | 480 | ANAPHYLATOXIN-LIKE 1. |
| FT | DOMAIN | 488 | 519 | ANAPHYLATOXIN-LIKE 2. |
| FT | DOMAIN | 521 | 553 | ANAPHYLATOXIN-LIKE 3. |
| FT | DOMAIN | 604 | 645 | EGF-LIKE 1, CALCIUM-BINDING. |
| FT | DOMAIN | 679 | 718 | EGF-LIKE 2. |
| FT | DOMAIN | 719 | 763 | EGF-LIKE 3, CALCIUM-BINDING. |
| FT | DOMAIN | 764 | 809 | EGF-LIKE 4, CALCIUM-BINDING. |
| FT | DOMAIN | 810 | 857 | EGF-LIKE 5, CALCIUM-BINDING. |
| FT | DOMAIN | 858 | 900 | EGF-LIKE 6, CALCIUM-BINDING. |
| FT | DOMAIN | 901 | 942 | EGF-LIKE 7, CALCIUM-BINDING. |
| FT | DOMAIN | 943 | 981 | EGF-LIKE 8, CALCIUM-BINDING. |
| FT | DOMAIN | 982 | 1024 | EGF-LIKE 9, CALCIUM-BINDING. |
| FT | DOMAIN | 1025 | 1069 | EGF-LIKE 10, CALCIUM-BINDING. |
| FT | DOMAIN | 1070 | 1184 | DOMAIN III. |
| FT | DISULFID | 445 | 472 | BY SIMILARITY. |
| FT | DISULFID | 446 | 479 | BY SIMILARITY. |
| FT | DISULFID | 459 | 480 | BY SIMILARITY. |
| FT | DISULFID | 489 | 518 | BY SIMILARITY. |
| FT | DISULFID | 502 | 519 | BY SIMILARITY. |
| FT | DISULFID | 521 | 545 | BY SIMILARITY. |
| FT | DISULFID | 522 | 552 | BY SIMILARITY. |
| FT | DISULFID | 535 | 553 | BY SIMILARITY. |
| FT | DISULFID | 608 | 620 | BY SIMILARITY. |
| FT | DISULFID | 616 | 629 | BY SIMILARITY. |
| FT | DISULFID | 631 | 644 | BY SIMILARITY. |
| FT | DISULFID | 683 | 693 | BY SIMILARITY. |
| FT | DISULFID | 689 | 702 | BY SIMILARITY. |
| FT | DISULFID | 704 | 717 | BY SIMILARITY. |
| FT | DISULFID | 723 | 736 | BY SIMILARITY. |
| FT | DISULFID | 730 | 745 | BY SIMILARITY. |
| FT | DISULFID | 751 | 762 | BY SIMILARITY. |
| FT | DISULFID | 768 | 781 | BY SIMILARITY. |
| FT | DISULFID | 775 | 790 | BY SIMILARITY. |
| FT | DISULFID | 796 | 808 | BY SIMILARITY. |
| FT | DISULFID | 814 | 827 | BY SIMILARITY. |
| FT | DISULFID | 821 | 836 | BY SIMILARITY. |
| FT | DISULFID | 843 | 856 | BY SIMILARITY. |
| FT | DISULFID | 862 | 875 | BY SIMILARITY. |
| FT | DISULFID | 869 | 884 | BY SIMILARITY. |
| FT | DISULFID | 886 | 899 | BY SIMILARITY. |
| FT | DISULFID | 905 | 917 | BY SIMILARITY. |
| FT | DISULFID | 913 | 926 | BY SIMILARITY. |
| FT | DISULFID | 928 | 941 | BY SIMILARITY. |
| FT | DISULFID | 947 | 956 | BY SIMILARITY. |
| FT | DISULFID | 952 | 965 | BY SIMILARITY. |
| FT | DISULFID | 967 | 980 | BY SIMILARITY. |
| FT | DISULFID | 986 | 998 | BY SIMILARITY. |
| FT | DISULFID | 994 | 1007 | BY SIMILARITY. |
| FT | DISULFID | 1009 | 1023 | BY SIMILARITY. |
| FT | DISULFID | 1029 | 1042 | BY SIMILARITY. |
| FT | DISULFID | 1036 | 1051 | BY SIMILARITY. |
| FT | DISULFID | 1056 | 1068 | BY SIMILARITY. |
| FT | CARBOHYD | 180 | 180 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 507 | 507 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 1035 | 1035 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| SQ | SEQUENCE | 1184 | AA; 126543 MW; CA48490A55F9EC5D | CRC64; |

Query Match 29.1%; Score 701.5; DB 1; Length 1184;
 Best Local Similarity 34.5%; Pred. No. 1e-44;
 Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      :| :|| | | :|:|:| :| :| | | :| | | |
Db      795 RCMDGF-LQDPEGNCVDINECTSLSEPCRPFGFSCINTVGSYTC----- 836

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHCNPTQIC 119
      |||| | | :| :|||:| | | :| | :|
Db      837 -----QRNPLICARGYHASDDGAKCVDVNECETGVHRCGEGQVC 875

Qy     120 INTEGgyTCSTdgyw--LLEGQCLDIDECRYG--YCQQLCANVPGSYSCTCNPGFTLN 174
      | | | | | :| :|:|:| | | | | | | | | |
Db     876 HNLPgsYRCdCKAGfQrDAfGRGcIDVNECWASpGRlCQHTCENTlGSYRCSCASgFLlA 935

Qy     175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC 233
      ||: |:|||| | :| | | | ||: | | ||: ||| |:|:| |: : ||
Db     936 ADGKRCEdVNECEaQR-CSQECANIgSYQCYCRQGYQLAEDGHTCTDIDeCAQgAGILC 994

Qy     234 QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDP 292
      |:| ||:| |:|| | | : : |||:|:| | | | : ||:|:| |:|:|
Db     995 TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R 1053

Qy     293 IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT 346
      | | |:| :| | | | | | | : : : | || | |:|
Db    1054 FECPPNYVQVSKTKC----ERTTCHDFLEcQNSPARITHYQLNfQTGLLVpAHIfRIGPA 1109

Qy     347 TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM 397
      : | | | | | :| : : : | : ||: ||:|
Db    1110 PAFTGDTIALNIiKGNEEGYfGTRRLNAYtGVVYLQRAVLEPRDFALdVEM 1160
  
```

RESULT 13

FBL1_HUMAN

ID FBL1_HUMAN STANDARD; PRT; 703 AA.
 AC P23142; P23143; P23144; P37888; Q8TBH8; Q9HBQ5; Q9UGR4; Q9UH41;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibulin-1 precursor.
 GN FBLN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
 RX MEDLINE=91100426; PubMed=2269669;
 RA Argaves W.S., Tran H., Burgess W.H., Dickerson K.;
 RT "Fibulin is an extracellular matrix and plasma glycoprotein with
 RT repeated domain structure.";
 RL J. Cell Biol. 111:3155-3164(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM D), TISSUE SPECIFICITY, AND INTERACTION
 RP WITH FN1 AND FGB.
 RX PubMed=9106159;

RA Tran H., Mattei M., Godyna S., Argraves W.S.;
 RT "Human fibulin-1D: molecular cloning, expression and similarity with
 RT S1-5 protein, a new member of the fibulin gene family.";
 RL Matrix Biol. 15:479-493(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM D).
 RX MEDLINE=99253993; PubMed=10318851;
 RA Krichevsky A.M., Metzger E., Rosen H.;
 RT "Translational control of specific genes during differentiation of
 RT HL-60 cells.";
 RL J. Biol. Chem. 274:14295-14305(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel Human cDNA clones with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
 RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
 RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Copley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
 RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaul S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chissole S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlffing T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,

RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
 RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
 RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
 RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.;
 RT "The DNA sequence of human chromosome 22.";
 RL Nature 402:489-495(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX PubMed=11829738;
 RA Castoldi M., Chu M.-L.;
 RT "Structural and functional characterization of the human and mouse
 RT fibulin-1 gene promoters: role of Sp1 and Sp3.";
 RL Biochem. J. 362:41-50(2002).
 RN [8]
 RP SEQUENCE OF 30-44.
 RX MEDLINE=89354537; PubMed=2527614;
 RA Argraves W.S., Dickerson K., Burgess W.H., Ruoslahti E.;
 RT "Fibulin, a novel protein that interacts with the fibronectin
 RT receptor beta subunit cytoplasmic domain.";
 RL Cell 58:623-629(1989).
 RN [9]
 RP SELF-ASSOCIATION AND INTERACTION WITH FN1.
 RX PubMed=1400330;
 RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,
 RA Argraves W.S.;
 RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding
 RT region of fibronectin.";
 RL J. Biol. Chem. 267:20120-20125(1992).
 RN [10]
 RP POSSIBLE FUNCTION.
 RX PubMed=7534784;

RA Roark E.F., Keene D.R., Haudenschild C.C., Godyna S., Little C.D.,
 RA Argraves W.S.;
 RT "The association of human fibulin-1 with elastic fibers: an
 RT immunohistological, ultrastructural, and RNA study.";
 RL J. Histochem. Cytochem. 43:401-411(1995).
 RN [11]
 RP INTERACTION WITH FGB.
 RX PubMed=7642629;
 RA Tran H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
 RA Argraves W.S.;
 RT "The interaction of fibulin-1 with fibrinogen. A potential role in
 RT hemostasis and thrombosis.";
 RL J. Biol. Chem. 270:19458-19464(1995).
 RN [12]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=8737292;
 RA Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;
 RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the
 RT early human embryo.";
 RL Histochem. J. 28:109-116(1996).
 RN [13]
 RP INDUCTION.
 RX MEDLINE=96133928; PubMed=8552629;
 RA Clinton G.M., Rougeot C., Derancourt J., Roger P., Defrenne A.,
 RA Godyna S., Argraves W.S., Rochefort H.;
 RT "Estrogens increase the expression of fibulin-1, an extracellular
 RT matrix protein secreted by human ovarian cancer cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:316-320(1996).
 RN [14]
 RP CALCIUM, SELF-ASSOCIATION, AND FN1-BINDING SITES.
 RX PubMed=9278415;
 RA Tran H., VanDusen W.J., Argraves W.S.;
 RT "The self-association and fibronectin-binding sites of fibulin-1 map
 RT to calcium-binding epidermal growth factor-like domains.";
 RL J. Biol. Chem. 272:22600-22606(1997).
 RN [15]
 RP ROLE IN TUMOR FORMATION AND INVASION.
 RX PubMed=9393974;
 RA Qing J., Maher V.M., Tran H., Argraves W.S., Dunstan R.W.,
 RA McCormick J.J.;
 RT "Suppression of anchorage-independent growth and matrigel invasion and
 RT delayed tumor formation by elevated expression of fibulin-1D in human
 RT fibrosarcoma-derived cell lines.";
 RL Oncogene 15:2159-2168(1997).
 RN [16]
 RP INDUCTION.
 RX PubMed=9811350;
 RA Roger P., Pujol P., Lucas A., Baldet P., Rochefort H.;
 RT "Increased immunostaining of fibulin-1, an estrogen-regulated protein
 RT in the stroma of human ovarian epithelial tumors.";
 RL Am. J. Pathol. 153:1579-1588(1998).
 RN [17]
 RP ROLE IN TUMOR FORMATION AND INVASION.
 RX PubMed=9466671;
 RA Hayashido Y., Lucas A., Rougeot C., Godyna S., Argraves W.S.,
 RA Rochefort H.;
 RT "Estradiol and fibulin-1 inhibit motility of human ovarian- and

RT breast-cancer cells induced by fibronectin.";
 RL Int. J. Cancer 75:654-658(1998).
 RN [18]
 RP INTERACTION WITH NOV.
 RX PubMed=9927660;
 RA Perbal B., Martinerie C., Sainson R., Werner M., He B., Roizman B.;
 RT "The C-terminal domain of the regulatory protein NOVH is sufficient to

Query Match 29.1%; Score 700; DB 1; Length 703;
 Best Local Similarity 34.7%; Pred. No. 8.1e-45;
 Matches 160; Conservative 65; Mismatches 148; Indels 88; Gaps 21;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      ||:||| | | |:||:| | | | | | | | | |
Db      293 QCKSGFIQD-ALGNCIDINECLSIAPCPIGHTCINTEGSYTC----- 334

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | | | | | | | | | | | | |
Db      335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 373

Qy      120 INTEGGYTCSDTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
      :|: | : | | | | : | :|:| | | | | | | | | | | |
Db      374 VNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS 433

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF 231
      |||||:|:|:|:|:|:| | | | | | | | | | | | | |
Db      434 VDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 492

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI 290
      :| : | :| | | :| | | | | : | :|:|:| | | | | | | |
Db      493 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGGFRCL 552

Qy      291 DPIRCEEPYLRISDN-----RCMCPAENPGCRDQPFTILYRDMDVVSGRSV----- 336
      | | | | : | | | | | | | | | | | | | | | |
Db      553 -AFCEPENYRRSAATLQQEKTDTVRCI-----KSCRPNDVTCVFDPVHTISHTVISLPTF 606

Qy      337 -----PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF-----YMRQTGPISATLVMTR 383
      | : | :| | :| | | | | | | | | | | | | | |
Db      607 REFTRPEEIIIFLRAITPPHPASQANIIFDITEGNLRDSFDI IKRYM--DGMTVGVVVRQVR 664

Qy      384 PIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
      || || | || | | | :| :| :|:|:| | |
Db      665 PIVGPFHAVLKLEMNYVVGGVVSHR--NVNVNRI FVSEYWF 703

```

RESULT 14

FBL1_MOUSE

ID FBL1_MOUSE STANDARD; PRT; 705 AA.
 AC Q08879; Q08878; Q8C3B1; Q91ZC9; Q922K8;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibulin-1 precursor (Basement-membrane protein 90) (BM-90).
 GN FBLN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS C AND D), AND LIGANDS INTERACTION.
 RX MEDLINE=93358897; PubMed=8354280;
 RA Pan T.-C., Kluge M., Zhang R.Z., Mayer U., Timpl R., Chu M.-L.;
 RT "Sequence of extracellular mouse protein BM-90/fibulin and its
 RT calcium-dependent binding to other basement-membrane ligands.";
 RL Eur. J. Biochem. 215:733-740(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC STRAIN=C57BL/6J; TISSUE=Head, and Urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX PubMed=11829738;
 RA Castoldi M., Chu M.-L.;
 RT "Structural and functional characterization of the human and mouse
 RT fibulin-1 gene promoters: role of Sp1 and Sp3.";
 RL Biochem. J. 362:41-50(2002).
 RN [5]
 RP CHARACTERIZATION OF NID AFFINITY.
 RX PubMed=7844816;
 RA Sasaki T., Kostka G., Goehring W., Wiedemann H., Mann K., Chu M.-L.,
 RA Timpl R.;
 RT "Structural characterization of two variants of fibulin-1 that differ
 RT in nidogen affinity.";
 RL J. Mol. Biol. 245:241-250(1995).
 RN [6]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=8850569;
 RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
 RT "Fibulin-1 and fibulin-2 expression during organogenesis in the
 RT developing mouse embryo.";
 RL Dev. Dyn. 205:348-364(1996).
 RN [7]
 RP NID-BINDING SITE.
 RC STRAIN=129/Sv;
 RX PubMed=9299350;
 RA Adam S., Goehring W., Wiedemann H., Chu M.-L., Timpl R., Kostka G.;
 RT "Binding of fibulin-1 to nidogen depends on its C-terminal globular
 RT domain and a specific array of calcium-binding epidermal growth
 RT factor-like (EG) modules.";
 RL J. Mol. Biol. 272:226-236(1997).
 RN [8]
 RP BINDING TO LAMA2.
 RX PubMed=10022829;
 RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
 RT "Binding of the G domains of laminin alpha1 and alpha2 chains and
 RT perlecan to heparin, sulfatides, alpha-dystroglycan and several
 RT extracellular matrix proteins.";
 RL EMBO J. 18:863-870(1999).
 RN [9]
 RP INTERACTION WITH AGC1 AND CSPG2.
 RX PubMed=10400671;
 RA Asperberg A., Adam S., Kostka G., Timpl R., Heinegaard D.;
 RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
 RT versican.";
 RL J. Biol. Chem. 274:20444-20449(1999).
 RN [10]
 RP INTERACTION WITH NID.
 RX PubMed=11589703;

RA Ries A., Goehring W., Fox J.W., Timpl R., Sasaki T.;
 RT "Recombinant domains of mouse nidogen-1 and their binding to basement
 RT membrane proteins and monoclonal antibodies.";
 RL Eur. J. Biochem. 268:5119-5128(2001).
 RN [11]
 RP DOWN-REGULATION BY GLUCOCORTICOIDS.
 RX PubMed=11737251;
 RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
 RT "Glucocorticoids down-regulate the extracellular matrix proteins
 RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
 RL Eur. J. Haematol. 67:176-184(2001).
 RN [12]
 RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RX PubMed=11238726;
 RA Ohsawa I., Takamura C., Kohsaka S.;
 RT "Fibulin-1 binds the amino-terminal head of beta-amyloid precursor
 RT protein and modulates its physiological function.";
 RL J. Neurochem. 76:1411-1420(2001).
 RN [13]
 RP INTERACTION WITH E6, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
 RX PubMed=12200142;
 RA Du M., Fan X., Hong E., Chen J.J.;
 RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
 RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
 RN [14]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=11836357;
 RA Debeer P., Schoenmakers E.F.P.M., Twal W.O., Argraves W.S.,
 RA De Smet L., Fryns J.-P., Van De Ven W.J.M.;
 RT "The fibulin-1 gene (FBLN1) is disrupted in a t(12;22) associated with
 RT a complex type of synpolydactyly.";
 RL J. Med. Genet. 39:98-104(2002).
 CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
 CC May play a role in cell adhesion and migration along protein
 CC fibers within the extracellular matrix (ECM). Could be important
 CC for certain developmental processes and contribute to the
 CC supramolecular organization of ECM architecture, in particular to
 CC those of basement membranes.
 CC -!- SUBUNIT: Interacts with itself and with various extracellular
 CC matrix components such as FN1, LAMA1, LMA2, NID, AGC1, CSPG2 and
 CC type IV collagen. Interacts also with papillomavirus E6 proteins.
 CC Binding analysis demonstrated for isoform C a 100-fold stronger
 CC binding to the basement membrane protein NID than for isoform D.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=D;
 CC IsoId=Q08879-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=Q08879-3; Sequence=Not described;
 CC Name=B;
 CC IsoId=Q08879-4; Sequence=Not described;
 CC Name=C;
 CC IsoId=Q08879-2; Sequence=VSP_001386;
 CC Note=Conflict E -> A at position 571 of isoform C (Ref.1);
 CC -!- TISSUE SPECIFICITY: Detected in most organs (brain, heart, lung,
 CC spleen, liver and kidney). Neurons are the predominant source of

CC production in the brain. Not expressed significantly by astrocytes
 CC or microglia.
 CC -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin
 CC family contributes to the formation of molecularly distinct
 CC extracellular matrices already during early developmental stages
 CC of a large number of tissues. Increase expression at neonate stage
 CC in the brain. Expressed in interdigital regions of the handplate
 CC of a 12 dpc embryo and in the lateral perichondrial region.
 CC Similar expression persists in the 13 dpc handplate particularly
 CC in the perichondrial regions and apical aspects of the developing
 CC digits.
 CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
 CC synthesis.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 9 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

Query Match 29.0%; Score 699; DB 1; Length 705;
 Best Local Similarity 35.0%; Pred. No. 9.6e-45;
 Matches 159; Conservative 67; Mismatches 154; Indels 74; Gaps 21;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      ||:|| | | :||:| | :| | | | |
Db      295 QCKSGFIQD-ALGNCIDINECLSIAPCPVGQTCINTEGSYTC----- 336

Qy      61 TPYSGPYAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | : | : ||||| : : | |
Db      337 -----QKNVFN-----CGRGYHLNEEGTRCVDVDECSPPAEPCKGHHHC 375

Qy      120 INTEGGYTCSTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
      :| : | : | :| : | :||:| | | | | | | :| :| :| :| :| :| :| :| :|
Db      376 LNSPGSFRCECKAGFYFDGISRTCDINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS 435

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SEF 231
      |||||:|||| | || | | |||: | | ||| : ||| | :|||:
Db      436 VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 494

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI 290
      :| : | :| ||:| ||| | | : | :|||:| | | :| :| :| :| :| :| :| :| :|
Db      495 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL 554

Qy      291 DPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFTILYRDMDVVSGRSV-- 336
      | | | | :| ||: | | : | | | :| :| :| :| :| :| :| :| :|
Db      555 S-FECPENYRRSADTFRQEKTDTVRCIKSCRPNDEACVRDPVHTVSHTVISLPTFREFT 613

Qy      337 PADIFQMQATT-RYPG--AYYIFQIKSGNEGREFYM---RQTGPISATLVMTRPIKGP 390
      | :| :| :| | | | | | | | | :| :| :| :| :| :| :| :| :|
Db      614 PEEIIFLRAVTPLYPANQADIIFDITEGNLRDSFDIIKRYEDGMTVGTVVRQVRPIVGP 673

Qy      391 IQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
      | ||| : | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      674 AVLKLEMNYVLGGVVSHR--NVVNVHIFVSEYWF 705

```

RESULT 15

FBL1_BRARE

ID FBL1_BRARE STANDARD; PRT; 681 AA.
AC O42182; O42183;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-1 precursor.
GN FBLN1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS C AND D).
RA Zhang H.-Y., Lardelli M., Ekblom P.;
RT "Sequence of zebrafish fibulin-1 and its expression in developing
RT heart and other embryonic organs."
RL Dev. Genes Evol. 207:340-351(1997).
CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
CC May play a role in cell adhesion and migration along protein
CC fibers within the extracellular matrix (ECM). Could be important
CC for certain developmental processes and contribute to the
CC supramolecular organization of ECM architecture, in particular to
CC those of basement membranes.
CC -!- SUBUNIT: Interacts with itself and with various extracellular
CC matrix components such as FN1, LAMA1, NID, AGC1 and CSPG2.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=D;
CC IsoId=O42182-1; Sequence=Displayed;
CC Name=C;
CC IsoId=O42182-2; Sequence=VSP_007379;
CC -!- DEVELOPMENTAL STAGE: Isoform C is detected in the later blastula
CC period, 4 h after fertilization. Isoform D is not detected at this
CC stage, it first appears during the gastrula period in 8-h-old
CC embryos. Expression of both isoforms is then maintained throughout
CC development. During later developmental stages, prominent
CC expression is seen in regions where tissue compartments are
CC continuously moving in relation to each other.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC -!- SIMILARITY: Contains 9 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF013751; AAB80944.1; -.
DR EMBL; AF013752; AAB80945.1; -.
DR HSSP; P35555; 1EMN.

DR ZFIN; ZDB-GENE-990415-73; fb1n1.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001673; S_mold_repeat.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00104; ANATO; 2.
 DR SMART; SM00179; EGF_CA; 5.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Signal; Alternative splicing; Glycoprotein; Extracellular matrix;
 KW Repeat; EGF-like domain; Calcium-binding.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 681 FIBULIN-1.
 FT DOMAIN 29 63 ANAPHYLATOXIN-LIKE 1.
 FT DOMAIN 68 107 ANAPHYLATOXIN-LIKE 2.
 FT DOMAIN 108 139 ANAPHYLATOXIN-LIKE 3.
 FT DOMAIN 158 192 EGF-LIKE 1.
 FT DOMAIN 193 238 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 239 284 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 285 331 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 332 373 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 374 415 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 416 455 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 456 499 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 500 554 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 29 55 BY SIMILARITY.
 FT DISULFID 30 62 BY SIMILARITY.
 FT DISULFID 43 63 BY SIMILARITY.
 FT DISULFID 72 103 BY SIMILARITY.
 FT DISULFID 85 104 BY SIMILARITY.
 FT DISULFID 106 125 BY SIMILARITY.
 FT DISULFID 107 138 BY SIMILARITY.
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 FT DISULFID 162 171 BY SIMILARITY.
 FT DISULFID 167 176 BY SIMILARITY.
 FT DISULFID 178 191 BY SIMILARITY.
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 FT DISULFID 289 301 BY SIMILARITY.
 FT DISULFID 317 330 BY SIMILARITY.
 FT DISULFID 336 348 BY SIMILARITY.
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 FT DISULFID 359 372 BY SIMILARITY.
 FT DISULFID 378 390 BY SIMILARITY.
 FT DISULFID 386 399 BY SIMILARITY.
 FT DISULFID 401 414 BY SIMILARITY.
 FT DISULFID 420 429 BY SIMILARITY.

FT DISULFID 440 454 BY SIMILARITY.
 FT DISULFID 460 473 BY SIMILARITY.
 FT DISULFID 469 482 BY SIMILARITY.
 FT DISULFID 484 498 BY SIMILARITY.
 FT DISULFID 504 517 BY SIMILARITY.
 FT DISULFID 511 526 BY SIMILARITY.
 FT DISULFID 531 553 BY SIMILARITY.
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 542 681 RPRVDRADIIRCVKSCQHNDISCVLNPILSHSHTAISLPTF
 FT REFNKPEEIVFLRSPTPTHLPHMDSPEIVYDILEGNIQNSF
 FT DIIKRLDHGMIVGVVKQVRPLVGPVRTVLKLANMYVTNGVV
 FT SHRNIINVRIYVSEFWF -> RCERLSCNESNECMAFTRRI
 FT TYYQLTFPAKIPVPTDLFRMGPSNTALGDDIEVAIVDGNRD
 FT GFFAAKRLDHGGVLVLQKPIAWPQDFQIALEMKLKRFHLS
 FT IYLFKIRPVRHARRHQQR (in isoform C).
 FT /FTId=VSP_007379.
 SQ SEQUENCE 681 AA; 74459 MW; 175C966305A46699 CRC64;

Query Match 26.2%; Score 629.5; DB 1; Length 681;
 Best Local Similarity 32.8%; Pred. No. 1.3e-39;
 Matches 151; Conservative 64; Mismatches 160; Indels 85; Gaps 21;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
 || || | | :||:| | :| | | | :| :
 Db 270 QCAAGFIQD-ALGSCIDINECVSVTALSRG-QMCFNTVGSFICQRHS----- 314

 Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHCNPTQIC 119
 : | || :| :|||:|||| :| :|
 Db 315 -----VTCGRGYHLNAEGTRCVDIDECAGPDNSCD-GHGC 348

 Qy 120 INTEGgyTCsCTDGYWL--LEGQCLDIDECRYGY---CQQLCANVPGSYsCTCNPGFTL 173
 || | | | | : : | | | | | | | | | : | | | | :| || |
 Db 349 INLVGSYRCECRTGFIFNSISRSCEDIDECR-NYPGRLCAHKCENILGSYKCSCTAGFKL 407

 Qy 174 NEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SE 230
 : |||:| |||| : :|| | | |||: | ||:| : ||: | |:||:
 Db 408 ADDGRNCDDVNECES-SPCSQGCANVYGSYQSYCRRGYQLSDADGITCEDIDECALPTGG 466

 Qy 231 FLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTcYNLQGGFKC 289
 : | : | | ||:| :|| | | : |||||:| | :| : :|:|:| |||:
 Db 467 HICSYRCHNTPGSFHCTCPASGYTLAANGRSCQDIDeCLTGTHSCSESEsCFNIQGGFRC 526

 Qy 290 IDPIRCEEPYLRISDN-----RCM--CPAENPGCRDQPFTILYRDMDVVS----- 332
 : | | | | ||:| :| :| | | :|
 Db 527 LS-FDCPANYRRSGDTRPRVDRADIIRCVKSCQHNDISCVLNP--ILSHSHTAISLPTFR 583

 Qy 333 GRSVPADIFQMqATT-----RYPGAYYIFQIKSGNEGREFYMRQT---GPISATLVMTRP 384
 : | :| :|| :| :| | | :| :| :| :| :| :|
 Db 584 EFNKPEEIVFLRSPTPTHLPHMDSPEIVYDILEGNIQNSFDIIKRLDHGMIVGVVKQVRP 643

 Qy 385 IKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
 : || | | | | :|| :| :|||:| :|
 Db 644 LVGPVRTVLKLANMYVTNGVVSHR--NIINVRIYVSEFWF 681

Search completed: January 9, 2004, 12:34:07
 Job time : 11.713 secs

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:32:07 ; Search time 32.5385 Seconds
(without alignments)
3354.684 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % | Query | | | | |
|--------|-------|-----------------|----|--|--|-------------|
| No. | Score | Match Length DB | ID | | | Description |
| ----- | | | | | | |

| | | | | | | |
|----|--------|------|------|----|--------|--------------------|
| 1 | 1276.5 | 53.0 | 443 | 4 | Q96TF5 | Q96tf5 homo sapien |
| 2 | 1273.5 | 52.9 | 443 | 11 | Q9JM06 | Q9jm06 mus musculu |
| 3 | 1253.5 | 52.1 | 443 | 4 | Q9H3D5 | Q9h3d5 homo sapien |
| 4 | 1096.5 | 45.6 | 493 | 11 | Q8BPB5 | Q8bpb5 mus musculu |
| 5 | 960.5 | 39.9 | 387 | 11 | Q8K0J4 | Q8k0j4 mus musculu |
| 6 | 741.5 | 30.8 | 685 | 11 | Q922K8 | Q922k8 mus musculu |
| 7 | 741.5 | 30.8 | 685 | 11 | Q8C3B1 | Q8c3b1 mus musculu |
| 8 | 735.5 | 30.6 | 683 | 4 | Q8TBH8 | Q8tbh8 homo sapien |
| 9 | 731.5 | 30.4 | 1174 | 11 | Q99K58 | Q99k58 mus musculu |
| 10 | 721 | 30.0 | 598 | 6 | Q8MJJ9 | Q8mjj9 cercopithec |
| 11 | 713 | 29.6 | 704 | 13 | O73774 | O73774 gallus gall |
| 12 | 703.5 | 29.2 | 576 | 4 | Q9Y3V7 | Q9y3v7 homo sapien |
| 13 | 702.5 | 29.2 | 1231 | 4 | Q8IUI1 | Q8iui1 homo sapien |
| 14 | 701.5 | 29.1 | 1231 | 4 | Q8IUI0 | Q8iui0 homo sapien |
| 15 | 695 | 28.9 | 638 | 4 | Q8NBH6 | Q8nbh6 homo sapien |
| 16 | 674.5 | 28.0 | 495 | 4 | Q9HBQ5 | Q9hbq5 homo sapien |
| 17 | 629.5 | 26.2 | 681 | 13 | O42182 | O42182 brachydanio |
| 18 | 587 | 24.4 | 698 | 5 | Q9V4B8 | Q9v4b8 drosophila |
| 19 | 581.5 | 24.2 | 554 | 4 | Q9UH16 | Q9uh16 homo sapien |
| 20 | 547.5 | 22.7 | 1409 | 5 | Q9VS89 | Q9vs89 drosophila |
| 21 | 542 | 22.5 | 2673 | 4 | Q96SC3 | Q96sc3 homo sapien |
| 22 | 531 | 22.1 | 5636 | 4 | Q96RW7 | Q96rw7 homo sapien |
| 23 | 518.5 | 21.5 | 2872 | 11 | Q9WUH8 | Q9wuh8 rattus norv |
| 24 | 517.5 | 21.5 | 741 | 4 | Q96K89 | Q96k89 homo sapien |
| 25 | 516.5 | 21.5 | 1398 | 13 | Q8AXM6 | Q8axm6 xenopus lae |
| 26 | 516 | 21.4 | 1389 | 11 | Q8CG18 | Q8cg18 mus musculu |
| 27 | 516 | 21.4 | 1713 | 11 | Q8CG19 | Q8cg19 mus musculu |
| 28 | 514.5 | 21.4 | 1399 | 13 | Q8JFZ4 | Q8jfh4 xenopus lae |
| 29 | 512.5 | 21.3 | 3857 | 11 | O88840 | O88840 mus musculu |
| 30 | 512 | 21.3 | 1713 | 11 | O88349 | O88349 mus musculu |
| 31 | 511.5 | 21.3 | 2809 | 4 | Q96JP8 | Q96jp8 homo sapien |
| 32 | 510.5 | 21.2 | 787 | 11 | Q8K061 | Q8k061 mus musculu |
| 33 | 508 | 21.1 | 188 | 11 | Q8R1U8 | Q8rlu8 mus musculu |
| 34 | 507.5 | 21.1 | 708 | 13 | P87363 | P87363 gallus gall |
| 35 | 506.5 | 21.0 | 2906 | 11 | Q9WUH9 | Q9wuh9 rattus norv |
| 36 | 493.5 | 20.5 | 729 | 11 | Q8BNH3 | Q8bnh3 mus musculu |
| 37 | 491.5 | 20.4 | 937 | 5 | Q9BLJ1 | Q9blj1 ciona intes |
| 38 | 484.5 | 20.1 | 1963 | 6 | Q28019 | Q28019 bos taurus |
| 39 | 482.5 | 20.0 | 1764 | 11 | O35806 | O35806 rattus norv |
| 40 | 480.5 | 20.0 | 517 | 4 | Q9NP01 | Q9np01 homo sapien |
| 41 | 474 | 19.7 | 746 | 4 | Q96HB9 | Q96hb9 homo sapien |
| 42 | 474 | 19.7 | 893 | 6 | Q8MJK0 | Q8mjk0 cercopithec |
| 43 | 474 | 19.7 | 1256 | 4 | Q9NS15 | Q9ns15 homo sapien |
| 44 | 474 | 19.7 | 1382 | 4 | Q9H7K2 | Q9h7k2 homo sapien |
| 45 | 471.5 | 19.6 | 1095 | 11 | Q60784 | Q60784 mus musculu |

ALIGNMENTS

RESULT 1

Q96TF5

| | | | | |
|----|-------------|---|------|---------|
| ID | Q96TF5 | PRELIMINARY; | PRT; | 443 AA. |
| AC | Q96TF5; | | | |
| DT | 01-DEC-2001 | (TrEMBLrel. 19, Created) | | |
| DT | 01-DEC-2001 | (TrEMBLrel. 19, Last sequence update) | | |
| DT | 01-MAR-2003 | (TrEMBLrel. 23, Last annotation update) | | |


```

Qy      361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      || :||:| | :|| | |: ||| | ||||:|:|:|:|:| | ||:| | :|
Db      381 GNSQGDFYIRQINNVSAMLVLARPTGPREYVLDLEMTVMNSLSYRASSVLRLTVFVGA 440

Qy      421 YPF 423
      ||
Db      441 YTF 443

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RESULT 2

```

ID      Q9JM06          PRELIMINARY;          PRT;    443 AA.
AC      Q9JM06;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      EGF-containing fibulin-like extracellular matrix protein 2.
GN      EFEMP2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20435063; PubMed=10982184;
RA      Katsanis N., Venable S., Smith J.R., Lupski J.R.;
RT      "Isolation of a paralog of the Doyme honeycomb retinal dystrophy gene
RT      from the multiple retinopathy critical region on 11q13.";
RL      Hum. Genet. 106:66-72(2000).
DR      EMBL; AF109122; AAF65189.1; -.
DR      HSSP; P00736; 1APQ.
DR      MGD; MGI:1891209; Efemp2.
DR      InterPro; IPR000152; Asx_hydroxyl.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR001491; Thrbomoduln.
DR      Pfam; PF00008; EGF; 4.
DR      PRINTS; PR00907; THRMBOMODULN.
DR      SMART; SM00179; EGF_CA; 4.
DR      PROSITE; PS00010; ASX_HYDROXYL; 4.
DR      PROSITE; PS01186; EGF_2; 4.
DR      PROSITE; PS01187; EGF_CA; 6.
KW      EGF-like domain; Matrix protein.
SQ      SEQUENCE    443 AA;  49452 MW;  5AEC2A91048B336A CRC64;

```

Query Match 52.9%; Score 1273.5; DB 11; Length 443;
Best Local Similarity 52.0%; Pred. No. 4.3e-117;
Matches 220; Conservative 65; Mismatches 121; Indels 17; Gaps 3;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCPRTNPVYRGPYSNPYS 60
:
Db 38 ECTDGYEWDADSQHCRDVNECLTIPEACKGEMKCINHYGGYLCLPRSAAVINDLHG---- 93

Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFQYQMDESNQCVDVDECATDSHCNPTQICI 120
:
Db 94 ---EGPPPPAA-----HAQQPNPCPGYEPDEQESCVDVDECTOALHDCRPSODCH 141

Qy 61 TPYSGPYAAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 120
 ||| ||| :| | ||:| | ||||| | | :| |
 Db 94 ---EGPPPPAA-----HAQQPNPCPGYEPDEQESCVDVDECTOALHDCRPSODCH 141

Db 94 ---EGPPPPAA-----HAQQPNPCPQGYEPDEQESCVDVDECTOALHDCRPSODCH 141

Qy 121 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
 | | | : | | | : : | | | | | | | | | : | | | : | | |
 Db 142 NLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSC 201
 Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQ 240
 | | | | | | | | | : | | : | | | : | | | | | | | : | | : | | : | | :
 Db 202 VDVNECDMGAPCEQRCFNSYGTFLCRCNQGYELHRDGFSCSDIDECGYSSYLCQYRCVNE 261
 Qy 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
 | | : | | | | | | | | | | : | | | | | | | : | | : | | | | : | | :
 Db 262 PGRFSCHCPQGYQLL-ATRLCQDIDECETGAHQCEAQTCVNFHGGYRCVDTNRCVEPYV 320
 Qy 301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKS 360
 : | | | | : | | | | | | | : | | : | | | | : | | | | : | | | | : | | :
 Db 321 QVSDNRCLCPASNPLCREQPSSIVHRYMSITSERSVPADVFQIQATSVYPGAYNAFQIRS 380
 Qy 361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
 | | : | | : | | : | | : | | | | | | | : | | : | | : | | : | | :
 Db 381 GNTQGDFYIRQINNVSAMLVLARPVTPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGA 440
 Qy 421 YPF 423
 | |
 Db 441 YTF 443

RESULT 3

Q9H3D5

ID Q9H3D5 PRELIMINARY; PRT; 443 AA..
 AC Q9H3D5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibulin-like extracellular matrix protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seibold S., Marx M.;
 RT "Cloning of a new fibulin-like gene."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF124486; AAG45245.1; -.
 DR HSSP; P35555; 1EMN.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001491; Thrbomoduln.
 DR Pfam; PF00008; EGF; 3.
 DR PRINTS; PR00907; THRMBOMODULN.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 5.
 KW EGF-like domain; Matrix protein.
 SQ SEQUENCE 443 AA; 49535 MW; D91784BF36A8A060 CRC64;

Query Match 52.1%; Score 1253.5; DB 4; Length 443;
 Best Local Similarity 51.3%; Pred. No. 4e-115;
 Matches 217; Conservative 67; Mismatches 122; Indels 17; Gaps 4;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      :||:|::| | | |::|| |||||:|:| |::| |||||:|:| | :
Db      38 ECTDGYEWDPSQHCRDVNECLTIPEACKGEMKGINHYGGYLCLPRSAAVINDLHG---- 93

Qy     61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 120
      || | || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     94 ---EGP-PPPVPPAQHPN-----PCPPGYEPDDQDSCVDVDECAQALHRRPSQDCH 141

Qy    121 NTEGGYTCSTDGWYLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    142 NLSGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSC 201

Qy    181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    202 VDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSYSSYLCQYRCVNE 261

Qy    241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      || : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    262 PGRFSCHCPQGYQLL-ATRLCQDIDECESGAHQCEAQTCVNFHGGYRCVDTNRCVEPYI 320

Qy    301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      ::|:||||:| | | | | | | | | | | | | | | | | | | | | | | |
Db    321 QVSENRLCPASNPLCREQPSSIVHRYMTITSERMRPADVFQIQATSVPYPGAYNAFQIRA 380

Qy    361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      || : ||:| | : | | | | | | | | | | | | | | | | | | | | |
Db    381 GNSQGDFYIRQINNVSAMVLARPVTGPREYVLDLEMTMNSLMSYRASSVLRLLTVFVGA 440

Qy    421 YPF 423
      | |
Db    441 YTF 443
  
```

RESULT 4

Q8BPB5

ID Q8BPB5 PRELIMINARY; PRT; 493 AA.
 AC Q8BPB5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Epidermal growth factor-containing fibulin-like extracellular matrix
 DE protein 1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Xiphoid cartilage;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of

RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC031184; AAH31184.1; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF00008; EGF; 3.
 DR SMART; SM00181; EGF; 5.
 DR SMART; SM00179; EGF_CA; 5.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 5.
 KW Hypothetical protein.
 SQ SEQUENCE 387 AA; 43334 MW; EE88DC9D1422C1C7 CRC64;

Query Match 39.9%; Score 960.5; DB 11; Length 387;
 Best Local Similarity 48.3%; Pred. No. 2.7e-86;
 Matches 171; Conservative 56; Mismatches 122; Indels 5; Gaps 4;

| | | | |
|----|-----|--|-----|
| Qy | 71 | APPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPQTQICINTEGGYTCSC | 130 |
| | | : : : : : | |
| Db | 38 | ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRTDQVCINLRGSFTQC | 95 |
| Qy | 131 | TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE | 189 |
| | | | |
| Db | 96 | LPGYQKRGEQCVDIDECTVPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCVDINECDAS | 155 |
| Qy | 190 | NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPPTYFCSCP | 249 |
| | | | |
| Db | 156 | NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP | 215 |
| Qy | 250 | PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPLYLRISDNRCMC | 309 |
| | | : : : | |
| Db | 216 | QGYEVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDHYVLTSENRCVC | 273 |
| Qy | 310 | PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM | 369 |
| | | | |
| Db | 274 | PVSNTMCRELPQSIVYKYSIRSRSVPSDIFQIQATMIYANTINTFRIKSGNENGEFYL | 333 |
| Qy | 370 | RQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF | 423 |
| | | : : : : : : : : : | |
| Db | 334 | RQTSPVSAMLVLVKSLSGPREYIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSS | 387 |

RESULT 6

Q922K8

ID Q922K8 PRELIMINARY; PRT; 685 AA.
 AC Q922K8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to fibulin 1.
 GN FBLN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; BC007140; AAH07140.1; -.
 DR EMBL; AK035388; BAC29054.1; -.
 DR MGD; MGI:95487; Fbln1.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01821; ANATO; 3.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 KW EGF-like domain.
 SQ SEQUENCE 685 AA; 75283 MW; EF0D77D7F66B73B8 CRC64;

Query Match 30.8%; Score 741.5; DB 11; Length 685;
 Best Local Similarity 36.5%; Pred. No. 2.1e-64;
 Matches 158; Conservative 64; Mismatches 152; Indels 59; Gaps 16;

| | | | |
|----|-----|---|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS | 60 |
| | | : : : | |
| Db | 295 | QCKSGFIQD-ALGNCIDINECLSISAPCPVGQTCINTEGSYTC----- | 336 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC | 119 |
| | | : : : | |
| Db | 337 | -----QKNVPN-----CGRGYHLNEEGTRCVDVDECSPPAEPCGKGHHC | 375 |
| Qy | 120 | INTEGGYTCSTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN | 174 |
| | | : : : : : : : : | |
| Db | 376 | LNSPGSFRCCKAGFYFDGISRTCVDINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS | 435 |
| Qy | 175 | EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF | 231 |
| | | : : : | |
| Db | 436 | VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEIDICALPTGGH | 494 |
| Qy | 232 | LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI | 290 |
| | | : : : : : : : : | |
| Db | 495 | ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL | 554 |

| | | | | | | |
|----|-----|---------------|-----------------------------|----------------------------------|-------|-----|
| Qy | 291 | DPIRCEEPYLRI | SDNRC-MCPA-ENPGCRDQ | PFTILYRDMDVVSGRSVPADIFQM | QATTR | 348 |
| | | : | : | : | : | |
| Db | 555 | S-FECPENYRRS | ADTRCERLPCHENQEC | PRLLPRITYYHLSFPTNIQVPAVVFRMGPSSA | | 613 |
| Qy | 349 | YPGAYYIFQIKSG | NEGREFYMRQTGPISATLVMTRPIKGP | PREIQLDLEM--ITVNTVIN | F | 406 |
| | | : | : | : | : | |
| Db | 614 | VPGDSMQLAITAG | NEEGFFTTTRKVS | SHSGVVALTKPIPEPRDLLLTVKMDLYRHGT | VSSF | 673 |
| Qy | 407 | RGSSVIRLRI | YVS | | | 419 |
| | | : | : | | | |
| Db | 674 | ---- | VAKLFIFVS | | | 682 |

RESULT 7

Q8C3B1

```

ID      Q8C3B1      PRELIMINARY;      PRT;      685 AA.
AC      Q8C3B1;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Fibulin 1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RX      MEDLINE=22354683; PubMed=12466851;
RA      The FANTOM Consortium,
RA      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
DR      EMBL; AK086451; BAC39669.1; -.
SQ      SEQUENCE      685 AA;  75282 MW;  E38377D35B08C560 CRC64;

```

Query Match 30.8%; Score 741.5; DB 11; Length 685;
Best Local Similarity 36.5%; Pred. No. 2.1e-64;
Matches 158; Conservative 64; Mismatches 152; Indels 59; Gaps 16;

| | | | |
|----|-----|--|-----|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS | 60 |
| Db | 295 | QCKSGFIQD-ALGNCIDINECLSIAPCPVGQTCINTEGSYTC----- | 336 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC | 119 |
| Db | 337 | -----QKNVPN-----CGRGYHLNEEGTRCVDVDECSPPAEPCKGHHHC | 375 |
| Qy | 120 | INTEGGYTCSTGDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN | 174 |
| Db | 376 | LNSPGSFRCKCKAGFYFDGISRTCVDINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS | 435 |
| Qy | 175 | EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SEF | 231 |
| Db | 436 | VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH | 494 |

| | | | | | |
|----|-----|-----------------------------------|---|-------------|-----|
| Qy | 232 | LCQHECVNQPGTYFCS | CP-PGYILLDDNRSCQDINECEHRNHTCNLQQT | CYNLQGGFKCI | 290 |
| | | : | : | : | : |
| Db | 495 | ICSYRCINIPGSFQC | SCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL | | 554 |
| Qy | 291 | DPIRCEEPYLRISDNRC-MCPA-ENPGCRDQ | PFTILYRDMDVVSGRSVPADIFQM | QATTR | 348 |
| | | : | : | : | : |
| Db | 555 | S-FECPENYRRSADTRCERLPC | HENQECPRLLPRLITYYHLSFPTNIQVPAVVFRMG | PSSA | 613 |
| Qy | 349 | YPGAYYIFQIKSGNEGREFYMRQTGPISATLVM | TRPIKGPRIQLDLEM--ITVNTVIN | | 406 |
| | | : | : | : | : |
| Db | 614 | VPGDMSQLAITAGNEEGFFTTRKVS | SHSGVVALTKPIPEPRDLLLTVMKMDLYRHGT | VSSF | 673 |
| Qy | 407 | RGSSVIRLRIYVS | | | 419 |
| | | : | : | : | : |
| Db | 674 | ----VAKLFIFVS | | | 682 |

RESULT 8

```

Q8TBH8
ID   Q8TBH8          PRELIMINARY;          PRT;   683 AA.
AC   Q8TBH8;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Fibulin 1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022497; AAH22497.1; -.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR006209; EGF_like.
DR   Pfam; PF01821; ANATO; 3.
DR   Pfam; PF00008; EGF; 6.
DR   SMART; SM00104; ANATO; 3.
DR   SMART; SM00179; EGF_CA; 8.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR   PROSITE; PS00010; ASX_HYDROXYL; 4.
DR   PROSITE; PS01186; EGF_2; 3.
DR   PROSITE; PS01187; EGF_CA; 8.
KW   EGF-like domain.
SQ   SEQUENCE      683 AA;  74423 MW;  2665A3961B6403B4 CRC64;

Query Match          30.6%;  Score 735.5;  DB 4;  Length 683;
Best Local Similarity 35.7%;  Pred. No. 8.1e-64;
Matches 155;  Conservative 66;  Mismatches 152;  Indels 61;  Gaps 16.

```

Qy 1 QCTNGFDLDRQSGQCLDI DECR TI PEACRGDMMCVNQNGGYLCI PR TNPVYRG PYSNPYS 60

Db 293 QCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC----- 334

Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
: || | || : : | : ||||| : | |

Db 335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 373

Qy 120 INTEGGYTCSTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
: | : | | || : : | : ||| | | | : | : | : | : |

Db 374 VNSPGSFRCECKTGYYFDGISRMCDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS 433

Qy 175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF 231
| | | | : | : | : : | | | | | : | | | : | : | : | : |

Db 434 VDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 492

Qy 232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCI 290
: | : | : | | : | | | | : : | : | : | | | : | : | : | : |

Db 493 ICSYRCINIPGSFQCSCPSSGYRLAPNGSNCQDIDECVTGIHNCSINETCFNIQGGFRCL 552

Qy 291 DPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTR 348
| | | | : | | | | | | | : : | : | : | : |

Db 553 -AFECPENYRRSAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPAVVFRMGPSA 611

Qy 349 YPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRG 408
| | | | | | | : | | : : | : | : | : : | : | : |

Db 612 VPGDSMQLAITGGNEEGFFTTRKVSPPHSGVVALTKPVPEPRDL-----LLTVKMDLSRHG 666

Qy 409 ---SSVIRLRIYVS 419
| | : | : |

Db 667 TVSSFVAKLFIFVS 680

RESULT 9

Q99K58

ID Q99K58 PRELIMINARY; PRT; 1174 AA.

AC Q99K58;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Similar to fibulin 2.

GN FBLN2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC005443; AAH05443.1; -.

DR HSSP; P00736; 1APQ.

DR MGD; MGI:95488; Fbln2.

DR InterPro; IPR000020; Anaphylatoxin.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR Pfam; PF01821; ANATO; 2.

DR Pfam; PF00008; EGF; 6.

Db 581 GTVSSF----VAKLFIFVS 595

RESULT 11

O73774

ID O73774 PRELIMINARY; PRT; 704 AA.
AC O73774;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fibulin-1, isoform D.
GN FBLN1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120531; PubMed=9923656;
RA Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;
RT "Identification of chicken and C. elegans fibulin-1 homologs and
RT characterization of the C. elegans fibulin-1 gene.";
RL Matrix Biol. 17:635-646(1998).
DR EMBL; AF051399; AAC05387.1; -.
DR HSSP; P00742; 1HCG.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF00008; EGF; 6.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00179; EGF_CA; 8.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 8.
KW EGF-like domain.
SQ SEQUENCE 704 AA; 78137 MW; D47D5A30D5E42932 CRC64;

Query Match 29.6%; Score 713; DB 13; Length 704;
Best Local Similarity 35.1%; Pred. No. 1.4e-61;
Matches 160; Conservative 64; Mismatches 154; Indels 78; Gaps 21;

QY 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
|| ||| | | :|:|:| | :|:| | | | | :|
Db 294 QCMNGFIQD-ALGNCIDINECLSTNMPCPAGQICINTDGSYTC-QRISP----- 340
QY 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-SNQCVDVDECATDSHQCNPTQIC 119
| || :| :| ||||| :| | :|
Db 341 -----SCGRGYHLNEDGTRCVDVDECSSSDQPCGEGHVC 374
QY 120 INTEGgyTCSCTDGYW--LLEGQCLDIDECRY---GYCQQLCANVPGSYSCNPGFTLN 174
|| | | | | | :| :|:|:| | | | | | | | | :|
Db 375 INGPgNYRCECKSGYSFDVISRTCIDINECRYPGRLLCAHKCENTPGSYCYCTCTMGFKLS 434

Qy 175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF 231
 |||||:|:|:| : :| | | | | : | | : :| : | :|:|:
 Db 435 SDGRSCEDLNECES-SPCSQECANVYGSYQCYCRRGFQLSDIDGISCEDIDECALPTGGH 493

Qy 232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI 290
 :| :| ||:| :| | | : :|:|:|:| | : :|:|:|:|:|:|:
 Db 494 ICSFRCINIPGSFQCTCPSTGYRLAPNARNCQDIDECVAETHNCSFNETCFNIQGGFRCL 553

Qy 291 DPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFTILYRDMDVVSGRSV-- 336
 : | | | : | | : | : | : | : | : : : |
 Db 554 S-LECPENYRKSGDTRLEKTDITIRCIKSCRPNVDVNCVLDPVHTISHTVISLPTFREFTR 612

Qy 337 PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF-----YMRQTGPISATLVMTRPIKGP 388
 | :| :|:| | | | | | | | | | : :|:|:|:
 Db 613 PEEIIFLRAITPTYPANQADIIFDITEGNLRESFDIIKRYM--DGMTVGVRQVRPIVGP 670

Qy 389 REIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
 | ||| : |:| : : : |:|:| |
 Db 671 FHAILKLEMNYVMGGVVSHR--NIVNVHIFVSEYWF 704

RESULT 12

Q9Y3V7

ID Q9Y3V7 PRELIMINARY; PRT; 576 AA.
 AC Q9Y3V7;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKFZP586A1519.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL050095; CAB43267.1; -.
 DR HSSP; P00736; 1APQ.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Hypothetical protein; EGF-like domain.
 FT NON_TER 1 1
 SQ SEQUENCE 576 AA; 63274 MW; FF2F0E9B185D8AC3 CRC64;

Query Match 29.2%; Score 703.5; DB 4; Length 576;
 Best Local Similarity 34.5%; Pred. No. 9.5e-61;
 Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
 :| :|| | | :||:| :| | | :| | |
 Db 187 RCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC----- 228

Qy 61 TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHCNPTQIC 119
 :||| | | : :|||:| | | :| :|
 Db 229 -----QRNPLICARGYHASDDGTKCVDVNECETGVHRCGEGQVC 267

Qy 120 INTEGGYTCSDTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPFGFTLN 174
 | | | | | : | :|:| | | | | | :| | |
 Db 268 HNLPGSYRCDCKAGFQRDAFGRGCI DVNECWASPGRLCQHTCENTLGSYRCSASCASGFLLA 327

Qy 175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC 233
 ||: |:| ||| : | | | | | : | | | | | :|:| | : | |
 Db 328 ADGKRCEQDVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC 386

Qy 234 QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDP 292
 | :| ||:| | :| | | : : |||:|:| | | : :|:|:| | :|:
 Db 387 TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R 445

Qy 293 IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT 346
 | | :|:| :| | | | | | : : : | | | | :|:
 Db 446 FECPPNYVQVSKTKC----ERTTCHDFLECNSPARITHYQLNFQTGLLVPAHIFRIGPA 501

Qy 347 TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM 397
 : | | | | | : : : | : | : | :|
 Db 502 PAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLQRAVLEPRDFALDVEM 552

RESULT 13

Q8IUI1

ID Q8IUI1 PRELIMINARY; PRT; 1231 AA.
 AC Q8IUI1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibulin 2.
 GN FBLN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li D., Marian A.J., Roberts R.;
 RT "Identification of a novel alternatively spliced isoform of human
 RT fibulin-2 gene abundantly expressed in heart and genetic evaluation in
 RT patients with ARVD.";
 RL (In) Unknown A. (eds.);
 RL ABSTRACTS OF THE 52ND ANNUAL MEETING OF THE AMERICAN SOCIETY OF HUMAN
 RL GENETICS, pp.323-323, Unknown Publisher (2002).
 DR EMBL; AY130458; AAN05435.1; -.
 DR EMBL; AY130456; AAN05435.1; JOINED.
 DR EMBL; AY130457; AAN05435.1; JOINED.
 SQ SEQUENCE 1231 AA; 131853 MW; 0A75D1C27F258D48 CRC64;

Query Match 29.2%; Score 702.5; DB 4; Length 1231;
Best Local Similarity 34.5%; Pred. No. 2.9e-60;
Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

| | | | |
|----|------|--|------|
| Qy | 1 | QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGYYLCI | 60 |
| Db | 842 | RCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC----- | 883 |
| Qy | 61 | TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHQCNPTQIC | 119 |
| Db | 884 | -----QRNPLICARGYHASDDGXKCVDVNECETGVHRCGEGQVC | 922 |
| Qy | 120 | INTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGFTLN | 174 |
| Db | 923 | HNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENTLGSYRCSASCASGFLLA | 982 |
| Qy | 175 | EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECS-FSEFLC | 233 |
| Db | 983 | ADGKRCEQDVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC | 1041 |
| Qy | 234 | QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDP | 292 |
| Db | 1042 | TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R | 1100 |
| Qy | 293 | IRCEEPYLRI SDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT | 346 |
| Db | 1101 | FECPPNYVQVSKTKC---ERTTCHDFLECQNSPARITHYQLNFQTGLLVPAHIFRIGPA | 1156 |
| Qy | 347 | TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM | 397 |
| Db | 1157 | PAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLORAVLEPRDFALDVEM | 1207 |

RESULT 14

Q8 IUI O

ID Q8IUI0 PRELIMINARY; PRT: 1231 AA.

AC Q8IUI0;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Fibulin 2.

GN FBLN2 .

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Li D., Marian A.J., Roberts R.;

RT "Identification of a novel alternatively spliced isoform of human

RT fibulin-2 gene abundantly expressed in heart and genetic evaluation in
RT patients with ARVD.":

RL (In) Unknown A. (eds.);

RL ABSTRACTS OF THE 52ND ANNUAL MEETING OF THE AMERICAN SOCIETY OF HUMAN

RL GENETICS, pp.323-323, Unknown Publisher (2002).

DR EMBL; AY130459; AAN05436.1; -.

SQ SEQUENCE 1231 AA; 131790 MW; 95D69EB2082952A7 CRC64:

Query Match 29.1%; Score 701.5; DB 4; Length 1231;
 Best Local Similarity 34.5%; Pred. No. 3.6e-60;
 Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      :| :|| | | :|:|:| :| :| | | :| | | |
Db      842 RCMDGF-LQDPEGNCVDINECTSLSEPCRPFGFSCINTVGSYTC----- 883

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHQCNPTQIC 119
      ||| | | :| :|||:| | | :| | :|
Db      884 -----QRNPLICARGYHASDDGAKCVDVNECETGVHRCGEGQVC 922

Qy     120 INTEGgyTCsCTDgyw--LLEGQCLDIDECRYG---YCQQLCANVPGSYsCTCNPGFTLN 174
      | | | | | :| :|:|:| | | | | | | | | |
Db     923 HNLPGSYRCDCkAGFQRDAfGRGCIDVNECWASpGRLCQHTCENTLGSYRCSCASGFLLA 982

Qy     175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC 233
      ||: |:| ||| :| | | | |||: | | ||: ||| |:|:| |:| :|
Db     983 ADGKRCEdVNECEaQR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDeCAQGAGILC 1041

Qy     234 QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTcyNLQGGFKCIDP 292
      |:| ||:| |:| | | :| :| ||:|:| | | | :| |:|:| |:| |:|
Db    1042 TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R 1100

Qy     293 IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMqAT 346
      | | |:|:| :| | | | | | :| :| :| | | | |:|
Db    1101 FECPPNYVQVSKTKC----ERTTCHDFLEcQNSPARITHYQLNFQTGLLVPAHIFRIGPA 1156

Qy     347 TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM 397
      :| | | | | | :| :| :| :| :| | |:| |:|
Db    1157 PAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLQRAVLEPRDFALDVEM 1207
  
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RESULT 15

Q8NBH6

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ID   Q8NBH6          PRELIMINARY;          PRT;          638 AA.
AC   Q8NBH6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein NT2RP3003649.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA   Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA   Nagahari K., Sugano S., Isogai T.;
RT   "HRI human cDNA sequencing project.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK075566; BAC11705.1; -.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001881; EGF_Ca.
  
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DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00181; EGF; 9.
 DR SMART; SM00179; EGF_CA; 9.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 KW Hypothetical protein.
 SQ SEQUENCE 638 AA; 70577 MW; EBC0DE3147A7621F CRC64;

Query Match 28.9%; Score 695; DB 4; Length 638;
 Best Local Similarity 34.5%; Pred. No. 7.4e-60;
 Matches 159; Conservative 65; Mismatches 149; Indels 88; Gaps 21;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 60
      || :|| | | :||:| | :| | | | | |
Db      228 QCKSGFIQD-ALGNCIDINECLISAPCPIGHTCINTEGSYTC----- 269

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC 119
      : || | | : : | | | | | | : | |
Db      270 -----QKNVFN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 308

Qy      120 INTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
      :| : | | | | : | :|:| | | | | | | | | | | | | |
Db      309 VNSPGSFRCECKTGYYFDGISRMCDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS 368

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF 231
      |||||:|:|:|:|:|:| | | | | | | | | | | | | | |
Db      369 VDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 427

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCI 290
      :| : | :| | | | | | | | : | :| | | | | | | | :| :| :| :| :| :| :|
Db      428 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGGFRCL 487

Qy      291 DPIRCEEPYLRISDN-----RCMCPAENPGCRDQPFTILYRDMDVVSGRSV----- 336
      | | | | : | | | | | | | | | | | | | | | | |
Db      488 -AFECPENYRRSAATLQQEKTDTVRCI-----KSCRPNVDVTCVFDPVHTISHTVISLPTF 541

Qy      337 -----PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF-----YMRQTGPISATLVMTR 383
      | : | :| | :| | | | | | | | | | | | | | :| |
Db      542 REFTRP EEIIFLRAITPPHPASQANIIFDITEGNLRDSFDIIKRYM--DGMTVGVRQVR 599

Qy      384 PIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
      || || | || | | | :| :| :| :| :| :| :|
Db      600 PIVGPFHAVLKLEMNYVVGGVVSHR--NVNVNHIFVSEYWF 638
  
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Search completed: January 9, 2004, 12:36:57
 Job time : 33.5385 secs